# 10/649, 273

#### Swope, Sheridan

From:

Swope, Sheridan

Sent:

Wednesday, January 26, 2005 1:34 PM

To:

STIC-Biotech/ChemLib

Subject:

10/649,273

For 10/649,273, pls search and interference search:

SID 2, full-length, against the NT and AA data bases

SID 2, residues 148-414, against the NT and AA data bases

SID 2, residues 176-414, against the NT and AA data bases

Sheridan Swope, Ph.D.
Patent Examiner, AU 1652
Recombinant Enzymes
571-272-0943 (voice)
E02B71 Remsen Bld (Office)
E02C70 Remsen Bld (Mailbox)



# STIC Search Report Biotech-Chem Library

#### STIC Database Tracking Number: 143413

TO: Sheridan Swope

Location: REM-2B71/2C70

Art Unit: 1652

Thursday, February 17, 2005

Case Serial Number: 10/649273

From: Mary Jane Ruhl

**Location: Biotech-Chem Library** 

Remsen 1-A-62

Phone: 571-272-2524

maryjane.ruhl@uspto.gov

#### Search Notes

Examiner Swope,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl Technical Information Specialist STIC Remsen 1-A-62 Ext. 22524



#### STIC-Biotech/ChemLib

143413

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Swope, Sheridan

Sent:

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Sheridan Swope, Ph.D. Patent Examiner, AU 1652 Recombinant Enzymes 571-272-0943 (voice) E02B71 Remsen Bld (Office) E02C70 Remsen Bld (Mailbox)

STAFF USE ONLY

Searcher: \_\_\_\_\_\_
Searcher Phone: 2Date Searcher Picked up: \_\_\_\_
Date Completed: \_\_\_\_
Searcher Prep/Rev. Time: \_\_\_\_
Online Tirne: \_\_\_\_\_

Type of Search

NA Sequence: #\_\_\_\_\_

AA Sequence : #\_\_\_\_\_

Structure: #\_\_\_\_

Bibliographic:

Litigation:

Patent Family:

Other:\_

\*\*\*\*\*\*\*\*\*

# Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated

- accession number. permanent accession numbers. The new UniProt record may not contain the previous temporary numbers from the most recent version of UniProt. These sequences have been assigned new Please note that the curators of the UniProt database have purged some temporary accession
- accession number can be found by searching the old accession number in the UniProt Protein extension .rup) that can no longer be found in the database, the permanent record with the new If you encounter an accession number from an older search run against UniProt (results file Archive database (UniPARC) at

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher

include a copy of this attachment to assist any future Examiners or numbers. members of the public who may encounter UniProt temporary accession When submitting sequence search results for scanning into IFW, please Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches. Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions .rnpm and .rnpn

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions .rapm and .rapn

Because they contain data that is confidential, the results of Pending database searches should not be left in the case.

Copyright

4

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Minimum
Maximum
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# SUMMARIES

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Protein e	Protein e	Bacillus	Protein e	Protein e	E. faeciu	Photorhab	Klebsiell	Protein e	Haemophil	Haemophil	Pasteurel	Glycoprot	Escherich	Salmonell	Bacterial	Protein e	Protein e	Protein e	Protein e

# ALIGNMENTS

RESULT 1

#### ABG96478 IID ABG9 XX AC ABG9 XX XX DT 11-E XX XX Nove XX WHOTO XW Geni Gen Metalloprotease; MP-1; immune disorder; glutamate transport; cancer; motor neuron disorder; amyotrophic lateral sclerosis; ALS; diabetes; reproductive disorder; Kleinfelter's syndrome; germinal cell aplasia; genital wart; metabolic disorder; premature puberty; Kallman syndrome; Cushing's syndrome; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; Huntington's disease; Tourette syndrome; sepsis; liver disease; renal disease; immuned disorder; rheumatoid arthritis; acquired immunodeficiency syndrome; AIDS; pulmonary disease; pneumonia; emphysema; cystic fibrosis; vascular disorder; inflammatory disorder; neurological disorder. ABG96478 standard; protein; Novel human metalloprotease MP1. 11-DEC-2002 ABG96478; (first entry) 414 Å

Homo sapiens.

WO200272751-A2

19-SEP-2002.

05-FEB-2002; 2002WO-US003353

05-FEB-2001; 10-APR-2001; 2001US-0266518P. 2001US-0282814P.

(BRIM ) BRISTOL-MYERS SQUIBB CO.

Chen Ģ Feder J, Nelson TC, Duclos ٦, Krystek

WPI; 200 N-PSDB; 2002-723329/78. DB; ABS76635.

New isolated nucleic acid encoding MP-1 protein, useful for preventing, treating, or ameliorating diseases associated with aberrant metalloproteinase activity, e.g. immune, metabolic, inflammatory and neurological disorders.

Claim 5; Fig 1A-C; 473pp; English.

The invention describes an isolated nucleic acid molecule (I) encoding a metalloprotease (MP-1). (I) is useful for preventing, treating, or

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RESULT 2
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ID ABB8
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Cytostatic; antiarteriosclerotic; anti-HIV; antiallergic; anticon cerebroprotective; antiparkinsonian; nootropic; antiinflammatory; antiulcer; hepatotropic; gynaecological; antibacterial; virucide; protozoacide; antiparasitic; cell proliferative disease; pMOD; protein modification and maintenance molecule; immunogenic fragme

anticonvulsant;

SEQ ID

ĕ

autoimmune;

inflammatory

disease; neurological

fragment;

Human protein modification + maintenance molecule protein

01-MAY-2003

(first entry)

ABJ26654 standard; protein;

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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mao
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPLHHAKNCDFSFTGLQHVTDKI IMKKEKEEGI EKGQI LSSAADI AATVQHTMACHLVKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRALEILTNATQCTLLCPPPRLCTDNG
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The invention relates to an isolated polypeptide comprising: any of 28 CC sequences of 48-1256 amino acids; a natural amino acid sequence at least CC 90% identical to the 28 amino acids sequence, 94% identical to a sequence CC of 703 or 267 amino acids, 96% identical to a sequence of 414 amino CC the specification; or a biologically active or immunogenic fragment of CC the isolated polypeptide. The polypeptides and polymucleotides are useful CC in diagnosing, treating and preventing diseases or conditions associated With the decreased expression of protein modification and maintenance CC molecules (PMOD), such as cell proliferative diseases (e.g. cancer, CC allergies), neurological disorders (e.g. stroke, Parkinson's disease, CC endometriosis), autoimmune/inflammatory diseases (e.g. AIDS, CC endometriosis), developmental (e.g. ulcer, cirrhosis), reproductive (e.g. cancer, CC endometriosis), developmental (e.g. ulcer, cirrhosis), reproductive (e.g. concertions), concertions (e.g. bacterial, viral, parasitic, protozoal). These are also CC useful in assessing the effects of exogenous compounds on the expression CC useful in assessing the effects of exogenous compounds on the expression CC tragments are useful in screening compounds for effectiveness as agonist or antagonist of the polypeptides, or in altering the expression of the traget polynucleotide and compounds that specifically bind to or modulate CC the activity of the polypeptide. The microarray is useful in monitoring cof the invention protein interactions, drug-target interactions, and coffice invention.
                                                                                             Query Match
Best Local S
Matches 414
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06-JUL-2001; 2001US-0303445P.
11-JUL-2001; 2001US-0311442P.
09-AUG-2001; 2001US-0311442P.
24-AUG-2001; 2001US-0314592P.
29-AUG-2001; 2001US-0315992P.
03-MAY-2002; 2002US-0378205P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated human PMOD polypeptide and polynucleotide, useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant PMOD expression, e.g. cancer, AIDS, atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thangavelu K, Thangavelu K, Mason PM,
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                                                                                                                                                                                                                                     Sequence 414 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 63; Page 182-183; 225pp;
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Warren BA,
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lu K, Gietzen KJ,
                                                                                             Conservative
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                                                                                                 0
                                                                                          Score 2125; DB 6;
Pred. No. 2.2e-215;
; Mismatches 0;
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L, Yao MG;
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문 ð

MLILTKTAGVPFKPSKRKVYEFLRSFNFHPGTLFLHKIVLGIETSCDDTAAAVVDETGNV

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome mapping; tissue typing; gene therapy; neuroprotective; cytostatic; anorectic; cardiant; haemostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7TM; glycoprotease; immune disorder; IgA deficiency; allergy; arrhythmia; rheumatoid arrhritis; diabetes; atherosclerosis; cardiovascular disorder; hypertension; ischaemic heart diseorder, obesity; myocardial infarction; endothelial cell disorder, Grave's disease; psoriasis; brain disorder; Parkinson's disease; Alzheimer's disease; haematopoietic disorder; cerebral oedema; metabolic disorder; liver disorder; platelet disorder;
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                                                                                 "Non-transmembrane domain"
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                                                                                                                                                                                             "Non-transmembrane domain; cytoplasmic domain"
                                                                                                                                                                                                                                                                                                                                                           "Non-transmembrane domain;
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                                                                                                                                                                                                                                                                                                     "Glycoprotease domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to novel 38650, 28472, 5495, 65507, 81588 CC or 14354 nucleic acid molecules which encode adenosine deaminase, glyco-grotease or seven transmembrane domain (7TM) receptor family members.

CC Sequences of the invention are useful in diagnosing and treating cancer cor aberrant cellular proliferation and/or differentiation (e.g. colon or lung cancer), immune disorders (e.g. selective IgA deficiency, rheumatoid arthritis, diabetes, allergy), heart or cardiovascular disorders (e.g., hypertension, atherosclerosis, arrhythmias, ischaemic heart disease, compocardial infarction, thrombus) including endothelial cell disorders (e.g., psoriasis, Grave's disease), haematopoietic disorders, brain cc disorders (e.g. cerebral oedema, Parkinson's or Alzheimer's disease), call and metabolic disorders (e.g. disorders (e.g. disorders (e.g. diagnostic assays, prospective medicine (e.g. diagnostic assays, prospective medicine (e.g. diagnostic assays, prospective medicine calds may also be used in chromosome mapping, tissue typing and consider of the invention are also used in gene therapy. The present sequence is human glycoprocease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New 38650, 28472, 5495, 65507, 81588 or 14354 nucleic acid molecules, useful for diagnosing and treating cancer, immune, cardiovascular, hematopoietic, brain, pain, metabolic, liver or platelet disorders, and
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08-NOV-2000; 2000US-0246772P.
15-NOV-2000; 2000US-0249185P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                    PPLHHAKNCDFSFTGLQHVTDKIIMKXEKEEGIEKGQILSSAADIAATVQHTMACHLVKR
                                                                                                                                          QGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIK 240
                                                                                                                                                                                                                 ALSLGVGLSFSLQLVGQLKKPFIPIHHMEAHALTIRLTNKVEFPFLVLLISGGHCLLALV 180
                                                                                                                                                                                                                                                                 LGEAIHSQTEVHLKTGGIVPPAAQQLHRENIQRIVQEALSASGVSPSDLSAIATTIKPGL
                                                                                                                                                                                                                                                                                   LGEAIHSQTEVHLKTGGIVPPAAQQLHRENIQRIVQEALSASGVSPSDLSAIATTIKPGL
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THRAILFCKQRDLLPQNNÄVLVASGGVASNFYIRRALEILTNATQCTLLCPPPRLCTDNG
                                                 PPLHHAKNCDFSFTGLQHVTDKNNENRKQEEGIEKGQILSSAADIAATVQHTMACHLVKR
                                                                                                                        QGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIK
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             The invention describes isolated 38650, 28472, 5495, 65507, 81588 and CC 14354 nucleic acid molecules (I) and their encoded polypeptides (II). The CC 38650 nucleic acid molecule comprises a sequence encoding adenosine CC deaminase. The 28472 nucleic acid molecule comprises a sequence encoding CC a human glycoprotease. The 5495, 65507, 81588 and 14354 comprise CC sequences that encode a human seven transmembrane domain (7TM). The CC 38650, 28472, 5495, 65507, 81588 or 14354 nucleic acid and polypeptide CC with or at risk of developing a disorder, e.g. cancer or aberrant CC cellular proliferation and/or differentiation (e.g. breast, ovarian, CC prostate, colon or lung cancer), immune disorders, hematopoietic disorders, CC cardiovascular disorders, endothelial disorders, hematopoietic disorders, CC blood vessel disorders, brain disorders, pain and metabolic disorders, CC liver disorders or platelet disorders. These disorders include carcinoma, CC prostate of the colon 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 breast cancer; ovarian cancer; prostate cancer; colon cancer; lung cancer; immune disorder; heart disorder; cardiovascular disorder; lendothelial disorder; hematopoietic disorder; blood vessel disorder; brain disorder; pain; metabolic disorder; liver disorder; disbettes; platelet disorder; carcinoma; sarcoma; leukaemia; Hodgkin's disease; autoimmune disorder; hypertension; atherosclerosis; heart failure; myocardial infarction; ischaemic heart disease; Crohn's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New adenosine deaminase, glycoprotease and seven transmembrane domain nucleic acids and polypeptides, designated 38650, 28472, 5495, 65507, 81588 and 14354, useful for treating e.g. leukemias, Hodgkin's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-NOV-2000; 2000US-0246768P.
08-NOV-2000; 2000US-0246772P.
15-NOV-2000; 2000US-0249185P.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Fig 8A-B; 178pp; English.
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Matches 407
                                                                                                          08-NOV-2000; 2000US-0246768P.
08-NOV-2000; 2000US-0246772P.
15-NOV-2000; 2000US-0249185P.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; enzyme; cancer; aberrant cellular proliferation; differentiation; immune disorders; heart disorder; brain disorder; cardiovascular disorder; endothedial cell disorder; pain disorder; haematopoeitic disorder; blood vessel disorder; metabolic disorder; liver disorder; platelet disorder; glycoprotease.
                                                                                                                                                                                                                                                                                      09-JAN
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(LEIB/)
(KAPE/)
(GLUC/)
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LBIBY K R.
KAPELLER-LIBERMANN
GLUCKSMANN M A.
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The invention relates to an isolated 38650 (encoding adenosine CC deaminase), 28472 (encoding a dyxcoprotease), 5495 (encoding a 7 CC transmembrane receptor), 65507, 81588 or 14354 nucleic acid molecule (or CC a sequence which is at least 60% identical to the six nucleic acids or CC naturally occurring variants, or a DNA insert of the plasmid deposited CC with the American Type Culture Collection as Accession No. not defined in CC the specification, which encodes the amino acid sequence). Also included CC are a host cell containing the nucleic acids (used to produce the CC are a host cell containing the nucleic acids (used to produce the CC the polypeptide, and identifying a compound that binds to/modulates the CC activity of the polypeptide. The nucleic acid molecules, polypeptides and CC methods are useful for diagnosing, treating cancer, aberrant cellular CC cardiovascular disorders including endothelial cell disorders, pain CC cardiovascular disorders including endothelial cell disorders, pain and metabolic disorders are given in the specification). The present CC cardiovascular disorders are given in the specification). The present
                                         sequence is the Human glycoprotease encoded by cDNA 28472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated 38650, 28472, 5495, 65507, 81588 and 14354 nucleic molecules, useful for diagnosing, treating cancer, pain, or immu heart, endothelial cell, hematopoeitic, blood vessel, brain, met
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ð 밁 S 밁 ঠ 밁 S 밁 ð 밁 8 밁 8 Matches Query Match Best Local 361 301 301 241 241 181 181 121 121 407; 61 61 ... Н Similarity IMIAWNGIERLRAGIGILHDIEGIRYEPKCPLGVDISKEVGEASIKVPQLKÆGI 414 THRAILFCKQRDLLFQNNAVLVASGGVASNFYIRRALBILTNATQCTLLCPPPRLCTDNG PPLHHAKNCDFSFTGLQHYTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMACHLVKR QGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIK ALSIGVGLSFSLQLVGQLKKPFIFIHIMEAHALTIRLTNKVBFPFLVLLISGGHCLLALV ALSIGVGISFSLQIVGQIKKPFIFIHMEAHALTIRITNKVEFPFIVILISGGHCLIAIV LGEAIHSQTEVHLKTGGIVPPAAQQLHRENIQRIVQEALSASGVSPSDLSAIATTIKPGL MLILTKTAGVFFKPSKRKVYEFLRSFNFHPGTLFLHKIVLGIETSCDDTAAAVVDETGNV MLILIKTAGVFFKPSKRKVYEFLRSFNFHPGTLFLHKIVLGIETSCDDTAAAVVDETGNV THRAILFCKORDLLPONNAVLVASGGVASNFYIRRALBILTNATOCTLLCPPPRLCTDNG PPLHHAKNCDFSFTGLQHVTDKNNENRKQEEGIBKGQILSSAADIAATVQHTMACHLVKR QGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIK LGEATHSQTEVHLKTGGTVPPAAQQLHRENTQRTVQEALSASGVSPSDLSATATTTKPGL Conservative 98.3%; ω •• Score 2088; DB 6; Pred. No. 1.9e-211; Mismatches Indels 0 Gaps 180 240 300 300 240 120 360 360 180 120 60

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Yamamoto J,
                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases in which the gene is involved, or as target molecules for gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 364
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24-JAN-2002; 2002US-0350435P.
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                                          THRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRALEILTNATQCTLLCPPPRLCTDNG
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Hio Y, Otsuka K, Nagai K, Irie
Otsuka M, Nagahari K, Masuho Y;
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                                                       The invention describes an isolated nucleic acid molecule (I) encoding a CC metalloprotease (WP-1). (I) is useful for preventing, treating, or ameliorating a medical condition, particularly an immune disorder, an CC ameriorating a medical condition, particularly an immune disorder, an CC amyotrophic lateral sclerosis (ALS), its juvenile form or an ALS-like condition. The compositions and methods are also useful for disposing, prognosticating, treating, ameliorating and/or treating disorders (CC associated with MP-1 activity, e.g. diabetes, cancer, reproductive CC disorders (e.g. Kleinfelter's syndrome, genital warts, or germinal cell aplasia), metabolic disorders (e.g. premature puberty, Kalman syndrome, CC or Cushing's syndrome), neurodegenerative diseases (Alzheimer's disease, CC and renal disease, Huntington's disease or Tourette syndrome), liver and renal diseases, Huntington's disease or Tourette syndrome), liver and renal diseases and immune disorders (e.g. AIDS, rheumatoid arthritis CC or sepsis), pulmonary diseases (e.g. pueumonia, emphysema or cystic CC fibrosis) and vascular, inflammatory and neurological disorders (e.g. Alzheimer's disease or Parkinson's disease). This is the amino acid CC sequence of a metalloprotease MP1 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid encoding MP-1 protein, useful for preventing, treating, or ameliorating diseases associated with aberrant metalloproteinase activity, e.g. immune, metabolic, inflammatory and neurological disorders.
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10-APR-2001;
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Query Match Best Local Simi Matches 267;

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  Query Match
                                                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                         Sequence 409 AA;
                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 34191; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Venter JC,
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11-JUL-2000; 2000US-00614150
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DB; ABL13236.
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Best Local Similarity Matches 156; Conserv
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23-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N--KVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPEC
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99US-0136392P 99US-0137722P 99US-0137722P 99US-0137722P 99US-0137724P 99US-0138847P 99US-0139452P 99US-0139452P 99US-0139453P 99US-0139458P 99US-0139458P 99US-0139452P 99US-0139452P 99US-0139452P 99US-0139452P 99US-0139452P 99US-0139452P 99US-0139452P 99US-0139461P 99US-0139462P 99US-0139462P 99US-0140852P 99US-0140852P 99US-0144085P 99US-0144332P 99US-0144884P 99US-0144332P 99US-0144884P 99US-0144884P 99US-0144884P 99US-0144884P 99US-0144884P 99US-0145088P 99US-0145088P	99US-0132486P. 99US-0132863P. 99US-0134256P. 99US-0134218P. 99US-013421P. 99US-013470P. 99US-0134768P. 99US-0134768P. 99US-013523P. 99US-013523P. 99US-013522P.
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RESULT 11
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05-MAR-1999;
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                                                                                                                        BP1033405-A2
                                                                                                                                                     Arabidopsis thaliana.
                                                                                                                                                                                                  protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                   Arabidopsis thaliana protein fragment SEQ ID NO: 21029.
                                                                                                                                                                                                                                                                                                                                                        AAG19285 standard; protein; 444 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QILSSA-----ADIAATVQHTMACHLVKRTHRAILFCKQRDLLFQNNAVLVASGGVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --RSGGPAVEELALEGDAKSVKFNVPMKYHKDCNFSYAGLKTQVRLAIEAKE----IDAK 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKG
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                                                                                                                                                                                      sequence.
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ilarity 40.8%;
Conservative 5
                                                       200089-00101439
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#8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                PPP 430
                                                                                                                                                                                                                                                                                                         --RSGGPAVEELALEGDAKSVKFNVPMKYHKDCNFSYAGLKTQVRLAIEAKE----IDAK
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(first entry)
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99US-0160815P

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99US-0161404P

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99US-0161406P

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                                                                       protein; 463
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40.8%; Pre
---ive 57;
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Pred. No. 3.3e-60;
7; Mismatches 127;
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                                                                                                                                                                                                                                                                                                                 the ygjD family, after the name given to the Escherichia coli family member. These proteins are essential for the survival of both Gram negative and Gram positive bacteria, although no function has as yet been ascribed to these proteins. The ygjD proteins, fragments of ygjD proteins (for example, fragments encompassing one or more conserved ygjD motifs such as AAY52318-Y5284) and nucleotides encoding them can be used to identify antagonists and broad spectrum antibacterial compounds. These antagonists and compounds can be used to treat a wide range of bacterial infections. New antibiotics are urgently needed, as serious bacterial infections and antibiotic resistant strains are becoming increasingly prevalent. The proteins of the invention are essential proteins for bacterial viability, and represent new targets for antibiotics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel bacterial polypeptides used to identify broad spectrum antibiotics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arigoni F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9954470-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treatment; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana ygjD protein homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proteins AAY52202-Y52217 encompass a novel family of proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ygjD protein; e:
identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein; essential; Gram positive; Gram negative; conserved; motif;
tification; antagonist; antibacterial; antibiotic; broad spectrum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-013253/01
                              217
                                                                                                                  142
                                                                                     158
                                                                                                                                                                                                                                 al Similarity
145; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Fig 1; 55pp; English
                                                                            T-NKVBFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPEC
                                                                                                                ALDKANLTEKDLSAVAVTIGPGLSLCLRVGVRKARRVAGNFSLPIVGVHHMEAHALVARL
                                                                                                                                 ALSASGYSPSDLSAIATTIKPGLALSLGYGLSFSLQLYGQLKXPFIPIHHMEAHALTIRL
                                                                                                                                                                        463 AA;
--RSGGPAVEELALEGDAKSVKFNVPMKYHKDCNPSYAGLKTQVRLAIBAKB
                                                                                                                                                                                              IVLGIETSCDDTAAAVVDETGNVLGEAIHSQTEVHLKTGGIVPPAAQQLHRENIQRIVQE
                           STMSCGKAI PHI AKQCAMPHPDIKFFLHHAKKCDFSFTGLQHVTDKI IMKKBKBEGIBKG
                                                         VEQELS PPFMALL I SGGHNLLVLAHKLGQYTQLGTTVDDA I GEAFDKTAKWLGLDMH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Edgerton MD,
                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98GB-00008423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-EP002635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "ygjD conserved 152. .198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "ygjD conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "ygjD conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .131
                                                                                                                                                                                                                                                 29.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      resistance; drug target.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "ygjD conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Loferer
                                                                                                                                                                                                                                    61;
                                                                                                                                                                                                                                 Score 634; DB 3;
Pred. No. 1.8e-57;
1; Mismatches 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peitsch MC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               motif 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          motif 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       motif 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   motif 3"
                                                                                                                                                                                                                                                             Length 463;
                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                  48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 designated family
                                                                                                                                                                                                                                  Gaps
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   308
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ABG964
AC ABG96
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aberrant glutamate transport or motor neuron disorder, such as amyotrophic lateral sclerosis (ALS), its juvenile form or an ALS-like condition. The compositions and methods are also useful for diagnosing, prognosticating, treating, ameliorating and/or treating disorders associated with MP-1 activity, e.g. diabetes, cancer, reproductive disorders (e.g. Kleinfelter's syndrome, genital warts, or germinal cell aplasia), metabolic disorders (e.g. premature puberty, Kallman syndrome, or Cushing's syndrome), neurodegenerative diseases (Alzheimer's disease, Puntington's disease or Tourette syndrome), liver and renal diseases and immune disorders (e.g. AIDS, rheumatoid arthritis or sepsis), pulmonary diseases (e.g. pneumonia, emphysema or cystic fibrosis) and vascular, inflammatory and neurological disorders (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Metalloprotease; MP-1; immune disorder; glutamate transport; cancer; motor neuron disorder; amyotrophic lateral sclerosis; ALS; diabetes; reproductive disorder; Klainfelter's syndrome; germinal cell aplasia; genital wart; metabolic disorder; premature puberty; Kallman syndrome; Cushing's syndrome; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; Huntington's disease; Tourette syndrome; sepsis; liver disease; renal disease; immune disorder; rheumatoid arthritis; acquired immunodeficiency syndrome; AIDS; pulmonary disease; pneumonia;
                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes an isolated nucleic acid molecule (I) encoding metalloprotease (MP-1). (I) is useful for preventing, treating, or ameliorating a medical condition, particularly an immune disorder, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid encoding MP-1 protein, useful for preventing, treating, or ameliorating diseases associated with aberrant metalloproteinse activity, e.g. immune, metabolic, inflammatory and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-FEB-2001; 2001US-0266518P.
10-APR-2001; 2001US-0282814P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 50; 473pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-723329/78.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        emphysema; cystic fibrosis; vascular disorder; inflammatory disorder;
neurological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human metalloprotease MP1 fragment #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG96489 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neurological disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Feder J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --IRNRADIAASFORVAVLHLEEKCERAIDWALE---LEPSIKHMVISGGVASNKYVRLR 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Duclos F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
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RESULT 14
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Best Local
                the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang
Wall
                                                                                                                                                                                                                                                                                                                                                                      New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-PEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bordetella
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                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-MAR-2002; 2002WO-US009107.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein encoded by Prokaryotic essential gene #8461.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ELIT-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2003-029926/02.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELITRA PHARM
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Trawick
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                                                                                                                                                                                                                                                                                                                       SEQ ID NO 50858; 1766pp; English.
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     (7)
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identifying a compound that
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Carr G
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Pred. No. 3.8e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ohlsen
Forsyth
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  influences the
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Xu HH;
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  activity of
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
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                                                                                                                             Metalloprotease; MP-1; immune disorder; glutamate transport; cancer; motor neuron disorder; amyotrophic lateral sclerosis; ALS; diabetes; reproductive disorder; Kleinfelter's syndrome; germinal cell aplasia; genital wart; metabolic disorder; premature puberty; Kallman syndrome; Cushing's syndrome; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; Huntington's disease; Tourette syndrome; sepsis; liver disease; renal disease; immune disorder; rheumatoid arthritis;
                                  acquired immunodeficiency syndrome; AIDS; emphysema; cystic fibrosis; vascular disor neurological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 382 AA;
                                                                                                                                                                                                                                                                                                                                                                                                         Novel human metalloprotease associated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG96491 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 QQLHRENIQRIVQEALSASGVSPSDLSAIATTIKPGLALSLGVGLSFSLQLVGQLKKPFI 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VVAGGVGANALLRAHLARALKPLRAEAYFPPLSLCTDNGAMIAFAAAERVKAGLADLRE 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KIIMKKEKEEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KSAKIMGI-GYP-----GGPALARLAEQGDASRYDLPRPMLHSGDLDFSFSGLKTAVLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GIHHLEGHLLSPLLAEPRPEPPFVALLVSGGHTQLMLVDGVGRYELLGETLDDAAGEAPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIHHMEAHALTIRLTN-KVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RV--KAATRDGGELGE--QDRADLAAATQAAIVEVLAAKAIRAL---KQTGL-----RRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HPGPRTLVVNSAPMIILGFESSCDETGVAAVCTERGLLAHALHTQIAMHQEYGGVVPBLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                     pulmonary
                                                                     inflammatory
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The invention describes an isolated nucleic acid molecule (I) encoding a metalloprotease (MP-1). (I) is useful for preventing, treating, or ameliorating a medical condition, particularly an immune disorder, an aberrant glutemate transport or motor neuron disorder, such as amyotrophic lateral sclerosis (ALS), its juvenile form or an ALS-like condition. The compositions and methods are also useful for diagnosing, prognosticating, treating, ameliorating and/or treating disorders group rognosticating, treating, ameliorating and/or treating disorders associated with MP-1 activity, e.g. diabetes, cancer, reproductive disorders (e.g. Kleinfelter's syndrome, genital warts, or germinal cell aplasial, metabolic disorders (e.g. premature puberty, Kallman syndrome, or Cushing's syndrome), neurodegenerative diseases (Alzheimer's disease, Parkinson's disease and immune disorders (e.g. AIDS, rheumatoid arthritis or sepsis), pulmonary diseases (e.g. AIDS, rheumatoid arthritis or sepsis), pulmonary diseases (e.g. memphysema or cystic fibrosis) and vascular, inflammatory and neurological disorders (e.g. Alzheimer's disease or Parkinson's disease). This is the amino acid sequence of a metalloprotease MP1 associated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
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10-APR-2001; 2001US-0282814P.
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389
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                                                          LSASGVSPSDLSAIATTIKPGLALSLGVGLSFSLQLVGQLKKPFIPIHHMEAHALTIRLT 158
----KCPLGVDISKEVGEASIKVPQLKM 412
                                                                                                                                                                                                                                                                                                                                      GIHVGAAVEILASRASADGHLRYPIFLPNVPKANMNFDQIKGSYLNLLERLRKNSETSID
                                                                                                                                                                                                  -----IPDFCASLQNTVARHISSKLHIFFESLSEQEKLPKQ---LVIGGGVAANQYIF 313
                                                                                                                                                                                                                                                                                                                                                                                                    TMSGGKAIEHLAKQGN---RFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIE 274
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                                                                                                                                                                                                                                                                KGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNFYIR 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.7%; Score 524; DB 5; Length 421; 33.4%; Pred. No. 6.7e-46;
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> 문 368 IYAHARSDIGTDASSEI----IDTPRRKL 392

Search completed: February 16, 2005, 13:05:54 Job time : 91.25 secs

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1 MLILTKTAGVFFKPSKRKVY......DISKEVGEASIKVPQLKMEI 414
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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                              US-10-067-443-2
US-10-067-443-19
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US-10-067-443-28
US-10-067-443-28
US-09-540-236-2726
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US-09-543-681A-6513
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Sequence 2, Appli
Sequence 19, Appli
Sequence 22, Appli
Sequence 25, Appli
Sequence 4, Appli
Sequence 28, Appli
Sequence 7726, Ap
Sequence 17372, A
Sequence 17372, A
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Sequence 9221, Appli
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US-10-67-443-2
; Sequence 2, Application US/10067443
; Patent No. 6642041
     301 THRAILFCKQRDLLFQNNAVLVASGGVASNFYIRRALBILTNATQCTLLCFPFRLCTDNG 360
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28
93.5	93.5	94.5	94.5	96	97	97	97	97	97.5	100	109	181.5	204	319	338.5	359	362
4.4	4.4	4.4	4.4	4.5	4.6	4.6	4.6	4.6	4.6	4.7	5.1	8.5	9.6	15.0	15.9	16.9	17.0
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Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
5019, Ap	6933, Ap	3197, Ap	5050, Ap	-	6, Appli	6, Appli	v	5, Appli	12013, A	144, App	33046, A	4387, Ap	19489, A	728, App	6, Appli	4609, Ap	81, Appl

#### ALIGNMENTS

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360	THRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRALEILTNATQCTLLCPPPRLCTDNG 360	Оу 301	_
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300	PPLHHAKNCDPSPTGLQHVTDKI IMKKEKEEGI EKGQI LSSAADIAATVQHTMACHLVKR	Оу 241	_
240	QGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIK	Db 181	-
240	QGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIK	Qy 181	_
180	ALSLGVGLSFSLQLVGQLKKPF1P1HHMEAHALT1RLTNKVEFPFLVLL1SGGHCLLALV	Db 121	_
180	ALSLGVGLSFSLQLVGQLKKPFIPIHHMEAHALTIRLTNKVEFPFLVLLISGGHCLLALV	Oy 121	_
120	LGEAIHSQTEVHLKTGGIVPPAAQQLHRENIQRIVQEALSASGVSPSDLSAIATTIKPGL	Db 61	
120	LGEAIHSQTEVHLKTGGIVPPAAQQLHRENIQRIVQEALSASGVSPSDLSAIATTIKPGL	Qy 61	_
60	1 MJILTKTAGVFFKPSKRKVYEFLRSFNFHPGTLFLHKIVLGIETSCDDTAAAVVDETGNV	Db 1	_
60	1 MJILTKTAGVFFKPSKRKYYEFLRSFNFHPGTLFLHKIVLGIETSCDDTAAAVVDETGNV	Qy	_
0,	Query Match 100.0%; Score 2125; DB 4; Length 414; Best Local Similarity 100.0%; Pred. No. 1.4e-234; Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps	Query Match Best Local Matches 41	
	ORGANISM: Homo sapiens 0-067-443-2	ORGANISM: H US-10-067-443-2	_
	7 7	; LENGTH: 414	
	SOFTWARK OF DAKE THE NOOF OF A C	SOPTWARE.	
	FILING DATE: 2001-04-10	; PRIOR FILI	
	APPLICATION NUMBER: US 60/282,814		
	PILING DATE: 2001-02-05	PRIOR FILL	
	ILING DATE: 2002-02-05	; CURRENT F	
	CURRENT APPLICATION NUMBER: US/10/067,443	; CURRENT AI	
	TITLE OF INVENTION: SPINAL CORD, MP-1	; TITLE OF ;	
Y EXPRESSED	INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED	; TITLE OF 1	
	APPLICANT: Bristol-Myers Squibb Company	; GENERAL INFORMATION:	
	197:11401	THE PERSON OF TH	

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CURRENT APPLICATION NUMBER: US/10/067,443;
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 19
; Sequence 22, Application US/10067443
; Patent No. 6642041
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
                                                                                                     US-10-067-443-22
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; TYPE: PRT
; ORGANISM: homo sapiens
US-10-067-443-19
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PATENT NO. 6642041
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: SQUIBB ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 412; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MLILTKTÄGVFFKPSKRKVYEFLRSFNFHPETLFLHKIVLGIETSCDDTÄAÄVVDETGNV 60
                                                                                                                                                                              ISKEVGEASIKVPQLKMEI 439
                                                                                                                                                                                                    ISKEVGEASIKVPQLKMEI 414
                                                                                                                                                                                                                                                                                                                                                                                                            PPLHHAKNCDFSFTGLQHVTDKI IMKKEKEEGIFLISKVEQINI PGLCLKIAAHFCRYEK
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CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.0
SEQ ID NO 22
LENGTH: 267
TYPE: PAT
ORGANISM: homo sapiens
US-10-067-443-22
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                                                                                                                                                                                                              ; TYPE: PRT; ORGANISM: Arabidopsis thaliana US-10-067-443-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-067-443-3
                                                                                                                                                                                                                                                                                            APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED IN
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REPERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOPTWARE: Patentin version 3.0
SEQ ID NO 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/10067443
Patent No. 6642041
GENERAL INFORMATION:
                                                                                                                           Query Match 29.8%; Score 634; DB 4; Length 463; Best Local Similarity 37.9%; Pred. No. 1.8e-63; Matches 145; Conservative 61; Mismatches 129; Indels 48;
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                                                                                                                                                                                                                                                                              LENGTH: 463
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mes 267; Conserv
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                                                                    ALSASGVSPSDLSAIATTIKPGLALSLGVGLSFSLQLVGQLKKPFIPIHHMEAHALTIRL 157
                                         VVLGIETSCDDTAAAVVSPFNHLSSSC---RAELLVQYGGVAPKQABBAHSRVIDKVVQD 141
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; LENGTH: 179
; TYPE: PRT
; ORGANISM: homo s
US-10-067-443-25
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GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT FILING DATE: 2002-05-05
CURRENT FILING DATE: 2002-02-05
CURRENT FILING DATE: 2002-05-05
CURRENT FILING DATE: 2002-
                     GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED

TITLE OF INVENTION: SPINAL CORD, MP-1
                                                                                                                                                       Sequence 4, Application US/10067443 Patent No. 6642041
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Best Local :
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PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
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         FILE REFERENCE: D0073 NP
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Pred. No. 2e-54;
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                                                                                                                     ; TYPE: PRT ; ORGANISM: Caenorhabditis elegans US-10-067-443-29
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US-10-067-443-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-05-
Query Match
Best Local Similarity
Matches 130; Conserva
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Patent No. 6642041
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PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOPTWARE: PatentIn version 3.0
SEQ ID NO 4
                                                                                                                                                                                                                                           SEQ ID NO 28
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Best Local Similarity
                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOPTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/266,518 PRIOR FILING DATE: 2001-02-05
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CURRENT FILING DATE: 2002-02-05
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TYPE: PRT
ORGANISM: Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IYAHARSDIGTDASSEI----IDTPRRKL
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   Conservative
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24.7%; Score 524; DB 4; I
33.4%; Pred. No. 6.3e-51;
ative 77; Mismatches 146;
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      Indels
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APPLICANT: Gary L. Bureton et al.
APPLICANT: Gary L. Bureton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2726, Application Patent No. 6673910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 2726
LENGTH: 350
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                       23.6%; Score 501; DB 4; Length 350; Local Similarity 34.5%; Pred. No. 2e-48; res 126; Conservative 56; Mismatches 130. Trans-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         335 RALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDIEGIRYEP-----
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                                                                                                                                                                                                  IRLT--NKVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAFGDMLDKVARRLSLIK 212
                                                                                                                                                                                                                                                        FNEMLDQANITKSDIDAVAYTKGPGLIGALMTGALFGRTLAYGLGVPAVGVHHMEGHLLA 125
                                                                                                                                                                                                                                                                                         VQEALSASGVSPSDLSAIATTIKPGLALSLGVGLSFSLQLVGQLKKPFIPIHHMEAHALT 154
                                                                                                                                                                                                                                                                                                                       VIGLETSCDETGLAIYDSTMNGRGGVLSQVLYSQINLHATYGGVVPELASRDHIRKLVPL
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   IRRALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAG---
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                                                                      IEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNFY 332
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                                      -ATRADIAASFEYAVVDTLVKKCTKALQMTGIRQ-----LVVAGGVSANQT 284
                                                                                                           -GGPNIEKLAKNGNPHAYELPRPMQH-KGLDFSFSGMKTAIHNLIKDTPNAQS
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US-08-087-797-3
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Matches
                                                                                                             Sequence 3, Application US/08087797 Patent No. 5543312
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                                                                                          GENERAL INFORMATION:
APPLICANT: Mellors, Alan
APPLICANT: Lo, Reggie Y.C.
APPLICANT: Abdullah, Khalid M.
TITLE OF INVENTION: Pasteurella H
TITLE OF INVENTION: Glycoprotease
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FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17372
LENGTH: 401
TYPE: PRT
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US-09-252-991A-17372
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Patent No. 6551795
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Pseudomonas aeruginosa
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                                              NGIERLRAGLGILHDIEGIRYEPKCPL 392
                                                                                         ---KOTGL--KN---LVIAGGVSANQALRSGLEKMLGEMKGOVFYARPRFCTDNGAMIAY
                                                                                                                                     LFCKQRDLLPQNNAVLVASGGVASNFYIRRALEILTNATQCTLLCPPPRLCTDNGIMIAW 365
                                                                                                                                                                                        RPGLDFSFSGLKTFTLN-TWQRCVEAGDDSEQ---TRCDIALAFQTAVVETLLIKCRRAL
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AGCQRLLAG---QHDGPAISVQPRWPM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                      GENERAL INFORMATION:
APPLICANT: GARY BRETON
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
                                                                                                                                              Sequence 6513, Application US/09543681A Patent No. 6605709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 23.0%; Score 488; DB 1; Length 342; Best Local Similarity 35.4%; Pred. No. 6e-47; Matches 126; Conservative 51; Mismatches 155; Indels
CURRENT APPLICATION NUMBER: US/09/543,681A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Layton, Jr., Samuel G.
REGISTRATION NUMBER: 22807
REFERENCE/DOCKET NUMBER: 337
TELECOMMUNICATION INFORMATION:
TELEPHONE: 704 377 1561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: No. 5543312th Carolina
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                                                                                                                                                                                                                                                                                                                                             LEILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDIEGIRYEPKCPL 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
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Best Local Similarity 34.2%; Pred. No. 2.8e-46;
Matches 122; Conservative 55; Mismatches 149
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LENGTH: 357
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PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
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APPLICANT: Mellor
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                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                         APPLICATION NUMBER: US/08/087,797
FILING DATE: 14-JUL-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lo, Reggie Y.C.
APPLICANT: Abdullah, Khalid M.
APPLICANT: Abdullah, Khalid M.
TITLE OF INVENTION: Pasteurella Haemolytica
TITLE OF INVENTION: Glycoprotease
TITLE OF INVENTION: Gene and the Purified E
TELECOMMUNICATION INFORMATION: TELEPHONE: 704 377 1561
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                                   NAME: Layton, Jr., Samuel G.
REGISTRATION NUMBER: 22807
REFERENCE/DOCKET NUMBER: 337.
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STATE: No. 5543312th Carolina
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                                                                                                                                                                                                                                                                                                                                                   ZIP: 28234
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                                                                                                                                                                                                                                                                                                                                                                                                                                           1211 Bast Morehead Street,
                                                                                                                                                                                                                                                                                                                                                                        United States
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                                             3374-80
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FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-9
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 9221
LENGTH: 343
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
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Matches
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                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
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TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 TNKVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECS
                                                                                                                                                                                                                                                123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      al Similarity
120; Conserv
                                                                                                                     99
                                                                                                                                                                                               39 VLGIETSCDDTAAAVVDETGNVLGEAIHSQTEVHLKTGGIVPPAAQQLHRENIQRIVQEA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 LKEANLQPSDIDGIAYTAGPGLVGALLVGSTIARSLAYAWNVPALGVHHMEGHLLAPMLE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99 LSASGVSPSDLSAIATTIKPGLALSLGVGLSFSLQLVGQLKKPFIPIHHMBAHALTIRL- 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39 VLGIETSCDDTAAAVVDETGNVLGEAIHSQTEVHLKTGGIVPPAAQQLHRENIQRIVQEA 98
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DNPPAFPFVALLVSGGHTQLISVTGIGQYELLGESIDDAAGEAFDKTAKLLGL-DYP---
                                     TNKVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECS 217
                                                                                                                     LSASGVSPSDLSAIATTIKPGLALSLGVGLSFSLQLVGQLKKPFIPIHHMEAHALTIRL- 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ILSSAADIAATVOHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKGQ 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ILGIETSCDETGVAIYDEDKGLVANQLYSQIDMHADYGGVVPELASRDHIRKTLPLIQEA
                                                                             LKEAĞLTAKDIDAVAYTAGPĞLVGALLVĞATVGRALAFAWNVPAIPVHHMEGHLLAPMLE 128
                                                                                                                                                             VLGIETSCDETGIAIYDDQQGLLANQLYSQVKLHADYGGVVPELASRDHVRKTVPLIQAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLR 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---TKCDIAHAFQQAV-----VDTILIKCK-RALEQTGYKRLVMAGGVSANKQLRADL
                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                              22.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.4%; Score 475.5; DB 1; 35.8%; Pred. No. 1.5e-45; tive 47; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N
                                                                                                                                                                                                                                           51;
                                                                                                                                                                                                                                           Score 474.5; DB 4;
Pred. No. 2.1e-45;
51; Mismatches 152;
                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 325;
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US-09-107-532A-6609
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                                                                                                                            US-09-107-532A-6609
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GENERAL INFORMATION:
                                             Matches
                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 6609: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: ATINIELD, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-0:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...363
SEQUENCE DESCRIPTION: SEQ ID NO: 6609:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                    HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lynn A Doucette-Stamm TITLE OF INVENTION: NUCLBIC ACID
                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        218 TMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKGQ 277
37 KIVLGIETSCDDTAAAVVDETGNVLGEAIHSQTEVHLKTGGIVPPAAQQLHRENIQRIVQ 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAEMMQXRGGEVFYARPBFCTDNGAMIAYAGMVRLQTGA----KABLGVTVRPRWPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --QTRADIARAFEDAVVDTLMIKCRRA------LEQTGFKRLVMAGGVSANRTLRAK 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNN-AVLVASGGVASNFYIRRA 336
                                                                                                                                                                                      NAME/KBY:
                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
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                                                                                                                                                                                                                                 ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Waltham
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                                                                                                                                                                                                                                                                                                                                                       ENGTH: 363 amino acids
                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                   (781)893-8277
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                                                            22.2%;
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                                        Score 472; DB 4;
Pred. No. 4.5e-45;
9; Mismatches 123
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AND AMINO ACID SEQUENCES RELATING TO
FABCIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                             123;
                                                                                 Length 363;
                                             Indels
                                             32;
                                             Gaps
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                                                                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-987-121A-4
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GENERAL INFORMATION:
APPLICANT: Hoskins, Jo Ann
APPLICANT: Tang, Joseph Chiou-Chu
APPLICANT: Treadway, Patti Jean
TITLE OF INVENTION: Streptococcus
                                                                                                                                         Query Match
Best Local Similarity
Matches 116; Conserv
                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: X-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/987,121A
APPLICATION NUMBER: US/08/987,121A
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ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
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                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
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89
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                                                                      4 RYILAPETSCDETSVAVLKNDDELLSNVIASQIESHKRFGGVVPEVASRHHVEVITACIE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -SYPSGKEIDQLAHQGKDNYHF--PRAMIHEDNYDFSFSGLKSAFINLVHNAQQRGEDLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EALSASGVSPSDLSAIATTIKPGLALSIGVGLSFSLQLVGQLKKPFIFIHHMEAHALTIR 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KN-----DLAASFQASVIDVLITKTLRA---C-----QNYPVKQLVVAGGVAANQG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAV--LVASGGVASNFY 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indiana
                                                                                                                                             21.7%; Score 461; DB 3; Length 336; ilarity 34.5%; Pred. No. 7.3e-44; Conservative 58; Mismatches 132; Indels
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                                                                                                                                                                                                                                                                                                                                                 317-276-3334
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                                                                                                                                                                                                                                                                                                                                  4.
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                                                                                                                                                                                                             124 SVEPLEPPLLALLVSGGHTELVYVSEAGDYKIVGETRDDAVGEAYDKVGRVMGL------
L--ATBITOVNVIIPPLRLCGDNAGMIAYASVSEWN 315
                                LEILTNATQCTLLCPPPRICTDNGIMIA-----WN 366
                                                          QILSSAADIAATVOHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRA 336
                                                                                                                                                                       STMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKG 276
                                                                                                                                        -TYPAGREIDELAHOGHDI-YDPPRAMIKEDNLEFSFSGLKSAFINLHHNAE-----QKG
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Search completed: February 16, 2005, 13:10:24 Job time: 27.75 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                           2125
2090.5
2090.5
2090.5
                     1385
1385
1385
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1: /cgn2_6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

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10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

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16: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*

19: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
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US-10-012-140-2039
US-10-094-749-2039
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Sequence 2, Appli
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Sequence 19, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 5, Appli
Sequence 2, Appli
Sequence 22, Appl
Sequence 22, Appl
Sequence 22, Appl
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Sequence 23, Appl
Sequence 209259,
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е 67993,	6 65	e 57817,	e 52054,	e 58204,	11043,	Sequence 13780, A	e 68438,	e 78161,	e 75485	e 56695,	10304,		e 66200,		e 67227,	e 631	e 24,	e 28,	4,	e 28, App	e 4,	e 28,	e 4	e 508	e 25	e 25,	e 25,	e 25,	Sequence 113732,	æ	Sequence 3, Appli

#### ALIGNMENTS

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; TYPB: PRT
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US-10-067-443-2
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Publication No. US20030082782A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
NUMBER OF SEQ ID NOS: 71
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                                                               LGEAIRSQTEVRIATOGIVEVAQQUHRENIQRIVQEALSASGVSPSDLSAIATTIKPGL 120
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Sequence 2, Application US/10649273

Publication No. US20040043407A1

GENERAL INFORMATION:

APPLICANT: Briscol-Myers Squibb Company

TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1

FILE REFERENCE: D0073 CNT

CURRENT APPLICATION NUMBER: US/10/649,273

CURRENT FILING DATE: 2003-08-27

PRIOR APPLICATION NUMBER: US 60/266,518

PRIOR FILING DATE: 2001-02-05

PRIOR APPLICATION NUMBER: US 10/067,443

PRIOR APPLICATION NUMBER: US 10/067,443

PRIOR APPLICATION NUMBER: US 60/282,814

PRIOR APPLICATION NUMBER: US 60/282,814

PRIOR FILING DATE: 2001-04-10

NUMBER OF SEQ ID NOS: 71

SOFTWARE: PatentIn version 3.2

SEQ ID NO 2

LENGTH: 414

TYPE: PRT

ORGANISM: Homo sapiens
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                                                      THRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRALEILTNATQCTLLCPPPRLCTDNG
                                                                                                      PPLHHAKNCDFSFTGLQHVTDXIIMKKEKEEGIEKGQILSSAADIAATVQHTMACHLVKR
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Sequence 2. Application US/10651722

; Publication No. US20040048302A1

; GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

; TILE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE, MP-1

; FILE REFERENCE: D0073 DIV

; CURRENT APPLICATION NUMBER: US/10/651,722

; CURRENT FILING DATE: 2003-08-29

; PRIOR APPLICATION NUMBER: US 60/266,518

; PRIOR APPLICATION NUMBER: US 10/067,443

; PRIOR APPLICATION NUMBER: US 10/067,443

; PRIOR APPLICATION NUMBER: US 60/282,814

; PRIOR APPLICATION NUMBER: US 60/282,814

; PRIOR FILING DATE: 2001-04-10

; NUMBER OF SEQ ID NOS: 71

; SCOTTMARE: Patentin version 3.2
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US-10-651-722-2
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Sequence 19, Application US/10067443

Publication No. US20030082782A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A N
FILE REFERENCE: DO073 CNT
CURRENT APPLICATION NUMBER: US/10/649,273
CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.2
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                           US-10-649-273-19
; Sequence 19, Application US/10649273
; Publication No. US20040043407A1
                                    ; TYPE: PRT ; ORGANISM: homo sapiens US-10-649-273-19
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PRIOR APPLICATION NUMBER: US 60/282,814
-PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.0
SEQ ID NO 19
LENGTH: 439
  Query Match
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Best Local
                                                                                                LENGTH: 439
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Similarity 93.8%;
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  Score 2090.5;
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                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.2 SEQ ID NO 19
                                                                                                                                                                                         Matches 412; Conservative
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                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                          Query Match
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TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
FILE REPERENCE: D0073 DIV
CURRENT APPLICATION NUMBER: US/10/651,722
CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR PILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR PILING DATE: 2002-02-05
PRIOR PILING DATE: 2002-02-05
PRIOR PILING DATE: 2001-04-10
NUMBER: US 60/282,814
PRIOR PILING DATE: 2001-04-10
NUMBER: DECOLITOR US 10/067,814
PRIOR PILING DATE: 2001-04-10
                                                                                                                                                                                                                                                                                  LENGTH: 439
TYPE: PRT
ORGANISM: homo @
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93.8%; Pred. No. 4e-196;
stive 0; Mismatches
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FILE REFERENCE: 381552004900
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: 00/246,768
PRIOR FILING DATE: 2000-11-08
PRIOR PRICATION NUMBER: 60/246,772
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/246,772
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/249,185
PRIOR APPLICATION NUMBER: 60/249,185
PRIOR PILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 49
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 414
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Publication No. US20030009017A1
GENERAL INFORMATION:
APPLICANT: Leiby, Kevin R.
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Glucksmann, Maria A.
TITLE OF INVENTION: 38550, 28472, 5495, 65507, 81588, AND
TITLE OF INVENTION: 14354 METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local (
                                                                                                                                                                                                                                                                                                        Local Similarity nes 407; Conserv
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PPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMACHLVKR 300
                                                  QGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIK 240
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                                                                                                                                                                                                                                                                                                       98.3%; Score 2088; DB 14; Length 414; 98.3%; Pred. No. 6.4e-196; rative 3; Mismatches 4; Indels 0
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US-10-094-749-2039
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                                                                                                                                                                                                                                                                                                                                          Query Match 86.8%;
Best Local Similarity 99.2%;
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SUGIYAMA, TOMOY,
OTSUKI, TETSUJI
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SATO, HIROYUKI
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PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2039
LENGTH: 364
TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US00-03-12
CURRENT FILING DATE: 2002-03-12
FRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2002-01-24
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PPLHHAKNCDFSFTGLQHYTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMACHLVKR
                                                                          QGVSDFLLLGKSLDIAPGDMLDKVARRLPLIKHPECSTMSGGKAIEHLAKQGNRFHFDIK 240
                                                                                                 QGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIK 240
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YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
NAGAHARI, KENJI
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NAGAI, KBIICHI
IRIE, RYOTARO
TAMECHIKA, ICHIRO
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YAMAMOTO, JUN-ICHI
ISONO, YUUKO
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Pred. No. 3.8e-172;
0; Mismatches 3;
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CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
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                                                                                                                                                                                    Sequence 22, Application US/10649273 Publication No. US20040043407A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 65.2%; Score 1385; DB 14; Length Best Local Similarity 100.0%; Pred. No. 3.5e-127; Matches 267; Conservative 0; Mismatches 0; Indels
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        APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
FILE REFERENCE: D0073 CNT
CURRENT APPLICATION NUMBER: US/10/649,273
CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
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TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: STANDAL CORD, MP-1
PRIOR FILING DATE: 2002-02-05
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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 267
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-651-722-22
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US-10-651-722-22
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Publication No. US20040048302A1
GENERAL INFORMATION:
APPLICANT: Briscol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
FILE REFERENCE: D0073 DIV
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PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.2
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 65.2%; Score 1385; DB 15; Best Local Similarity 100.0%; Pred. No. 3.5e-127; Matches 267; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                              Matches 267; Conservative
                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
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CURRENT FILING DATE: 2003-08-29
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                                                                                                                                                                                                                                                                                      Local Similarity
268 EKEEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGV
                                                                                              208 LSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKK 267
                                                                                                                                                                                            148 MEAHALTIRLTINKVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARR 207
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                                                                        LSLI KHPECSTMSGGKAI EHLAKQGNRFHFDI KPFLHHAKNCDFSFTGLQHVTDKI IMKK
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US-10-424-599-209259
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Sequence 3, Application US/10067443
Publication No. US20030082782A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
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APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Cao Yinua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5322)B
CURRENT EPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 209259
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ORGANISM: Glycine max
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tch 32.1%; Score 681.5; DB 15; Length 445; al Similarity 43.1%; Pred. No. 8.8e-58; 155; Conservative 54; Mismatches 126; Indels 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQ-----HVTDKIIMKKEKEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                              GIEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNF 331
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                                                                                                                                                                                                                                                                                                      YVRARLDMVVKKNGLQLVCPPPRLCTDNGVMIAWTGIEHFRMG---
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                                                                                A NOVEL METALOPROTEASE HIGHLY EXPRESSED
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TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A N
FILE REFERENCE: DO073 CWT
CURRENT APPLICATION NUMBER: US/10/649,273
CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR PILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR PILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR PILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PATENTIN VETSION 3.2
SEQ ID NO 3
                                                                                          ; ORGANISM: Arabidopsis thaliana US-10-649-273-3
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TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-067-443-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-649-273-3
Query Match 29.8%; Score 634; DB 15; Best Local Similarity 37.9%; Pred. No. 4.3e-53; Matches 145; Conservative 61; Mismatches 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/10649273 Publication No. US20040043407A1 GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bristol-Myers Squibb Company
                                                                                                                                         TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDIEGIRYE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -- RSGGPAVEELALEGDAKSVKFNVPMKYHKDCNFSYAGLKTQVRLAIEAKE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         A NOVEL METALOPROTEASE, MP-1
                                            Length 463;
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Indels

48;

Gaps

7;

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; LENGTH: 463
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-651-722-3
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CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ś
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/10651722
Publication No. US20040048302A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
FILE REFERENCE: D0073 DIV
                                            217
                                                                                202 VEQELSPPFMALLISGGHNLLVLAHKLGQYTQLGTTVDDAIGEAPDKTAKWLGLDMH--- 258
                                                                                                                                                              277
259 -- RSGGPAVEBLALEGDAKSVKFNVPMKYHKDCNFSYAGLKTQVRLAIBAKB------ 308
                                                                                                         158 T-NKVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPEC 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202 VEQELSFPFMALLISGGHNLLVLAHKLGQYTQLGTTVDDAIGEAFDKTAKWLGLDMH--- 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 T-NKVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPEC 216
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                                                                                                                                                                                                                                               85 VVLGIETSCDDTAAAVVSPFNHLSSSC---RAELLVQYGGVAPKQAEBAHSRVIDKVVQD 141
                                                                                                                                                                                                                                                                    38 IVLGIETSCDDTAAAVVDETGNVLGEAIHSQTEVHLKTGGIVPPAAQQLHRENIQRIVQE 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRA 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----PKCPLGVDISKEVGEA 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LNNIVENKNLKLVCPPPSLCTDNGVMVAWTGLEHFRVG-----RYDPPPPATEPE 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --RSGGPAVEELALEGDAKSVKFNVPMKYHKDCNFSYAGLKTQVRLAIEAKE------ 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALDKANLTEKDLSAVAVTIGPGLSLCLRVGVRKARRVAGNFSLPIVGVHHMEAHALVARL 201
                                                                                                                                                                                                                                                                                                                               Gaps
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414 DYVYDLRPRWPLGEEYAKGRSEA 436 309 --IRNRADIAASFQRVAVLHLEEKCERAIDWALE---LEPSIKHMVISGGVASNKYVRLR 363 LEILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDIEGIRYB-----------PKCPLGVDISKEVGEA 403

Search completed: February 16, 2005, 13:28:29 Job time : 242.85 secs

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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Maximum Match 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title:
Perfect score:
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Pending Patents AA Main:*

1: /cgm2=6/ptodata/1/paa/US06_COMB.pep:*
2: /cgm2=6/ptodata/1/paa/US06_COMB.pep:*
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4: /cgm2=6/ptodata/1/paa/US081_COMB.pep:*
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9: /cgm2=6/ptodata/1/paa/US083_COMB.pep:*
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18: /cgm2=6/ptodata/1/paa/US093_COMB.pep:*
19: /cgm2=6/ptodata/1/paa/US103_COMB.pep:*
19: /cg
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2125
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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634	634	634	634	000	9		•			714.5	714.5	•	٠	82	N	1385	1385	1385	1385	8	æ	æ	9	1395	9	1395	1395	1395	1395	1845	2088	2090.5	•	•	•	•	2125	2125	2125	2125	2125	2125	2125	2125	2125	Score
29.8	29.8	29.8	٠.	30.9	٠	٠:	٠:	ا د	u	33.6	33.6	Ψ	۳	8				5	'n	ŗ	65.2	5	5		5	5	•	65.6			98.3	98.4	98.4		98.4	98.4	•	•	•	•	100.0	8	•	•	100.0	
463	463	463	463	461			2 4	445	409	409	409	409	408	291	291	267	267	267	267	267	267	267	309	309	309	309	298	298	298	364	414	439	439	439	439	439	425	425	414	414	414	414	414	414	414	Length
32	32	21	<u> </u>	ي ،				ا بر	37	37	20	20	37	37	37	37	37	37	35	32	32	_	37	37	<u>3</u> 5	35	37	35	27	26	26	37	37		32	<b>,_</b>	37	35	37		32	32	30	۳	۳	BB
10-651-722-	US-10-649-273-3	09-708-427-	US02-03353-3	TO-449-902-	09-513-996A-210	09-313-9968-2103	700000000000000000000000000000000000000	-10-424-599-20925	-60-191-6	-60-191-63	US-09-614-150A-34191	-09-614-15	-60-173-4	-60-243-742-177	-60-243	-60	-60-282	-60-266-518-	-10-918-754-	-10-651-722-22	-10-649-273-2	-US02-03353-	-60-495-114-1	-60-495-114-	-10-918-754-	754-	-60-495-114-	-10-918-754-	-10-170-205E-	-10-094-749-	-10-012-140-	-60-282-814-1	-60-266-518-1	-10-651-722-1	-10-649-273-1	-US02-03353-1	-60-495-114-13	-10-918-754-137	-60-282-814-	-60-266-51	-10-651-722-	S-10-649-273-	-10-48	CT-US02-1936	PCT-US02-03353-2	ID
Ψ	Sequence 3, Appli	6	Appii	sequence 4898/,	equence 21029,		3100				Sequence 34191, A		26192	177,	101	13	22,	22,	137	22,	e 22,	22, A	1375,	1374,	equence 1375,	1374,	1371,		27	N	'n	19	19	e 19,	e 19,	19, Apr	1372	1372,	2		2	e 2,	е 8,	e 8, 7	quence 2,	iption

## ALIGNMENTS

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Sequence 2, Application PC/TUS0203353

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
PILE REPERENCE: D0073 PCT
CURRENT APPLICATION NUMBER: PCT/US02/03353
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR PILING DATE: 2001-02-05
PRIOR PILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR PILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SCOPTMANE: PATCHILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SEQTIANE: PATCHILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 1
PCT-US02-03353-2
ORGANISM: Homo sapiens
                                      LENGTH: 414
TYPE: PRT
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; Sequence 8, Application PC/TUS0219360
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: KABLE, Amy E.
; APPLICANT: KABLE, Amy E.
; APPLICANT: SWARNAKAR, Anita
; APPLICANT: HAPALIA, April J.A.
; APPLICANT: TRAN, Bao
; APPLICANT: DUGGAN, Brendan M.
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                             YAO, Monique G.
WALIA, Narinder K.
MASON, Patricia M.
GURURAJAN, Rajagopal
LEE, Sally
BECHA, Shanya D.
LEE, Soo Yeun
                                                                                                                                                                                                                                                                                                                                  DUGGAN, Brendan M. WARREN, Bridget A. ISON, Craig H. HONCHELL, Cynthia D. NGUYEN, Danniel B.
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                                                                                                                                BAUGHN, Mariah R. BOROWSKY, Mark L.
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THANGAVELU, Ka
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GRIFFIN, Jennifer A.
                                                                                                                                                                                                                                                              FORSYTHE, Ian
BARROSO, Ines
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E, Ernestine A.
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                   Uyen K.
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RESULT 3
US-10-480-988-8
; Sequence 8, Application US/10480988
; GENERAL INFORMATION:
; APPLICANT: GANDHI, Ameena R.; KABLE, Amy E.;
APPLICANT: SWARNAKAR, Anita; HAFALIA, April
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PRIOR APPLICATION NUMBER: US 60/30,508
PRIOR PILING DATE: 2001-06-22
PRIOR PILING DATE: 2001-06-62
PRIOR APPLICATION NUMBER: US 60/303,445
PRIOR APPLICATION NUMBER: US 60/303,445
PRIOR APPLICATION NUMBER: US 60/305,405
PRIOR PILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/311,442
PRIOR PILING DATE: 2001-08-09
PRIOR PILING DATE: 2001-08-24
PRIOR PILING DATE: 2001-08-24
PRIOR PILING DATE: 2001-08-29
PRIOR PILING DATE: 2001-08-29
PRIOR PILING DATE: 2002-08-29
PRIOR PILING DATE: 2002-08-29
PRIOR PILING DATE: 2002-08-29
PRIOR PILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PERL PROGRAM
SEQ ID NOS: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7632424CD1
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Best Local
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APPLICANT: SPRAGUE, William
APPLICANT: TANG, Y. Tom
APPLICANT: LU, Yan
APPLICANT: LU, Yan
APPLICANT: ZEBARJADIAN, Yeganeh
TITLE OF INVENTION: PROTEIN MODIFICATION AND MAINTENANCE MOLECULES
FILE REFERENCE: PF-1040 PCT
CURRENT APPLICATION NUMBER: PCT/US02/19360
CURRENT FILING DATE: 2002-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 414
TYPE: PRT
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                                                                                                                                             ALSIGVGLSFSIQIVGQLKKPFIPIHMEAHALTIRITNKVEFPFLVLLISGGHCLLALV
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IMIAWNGIERLRAGIGILHDIEGIRYEPKCPLGVDISKEVGEASIKVPQLKMEI
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April J.A.;

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APPLICANT: YUE, Henry; FORSYTHE, Ian J.;
APPLICANT: BARROSO, Ines; RAMKUMAR, Jayalaxmi;
APPLICANT: BARROSO, Ines; RAMKUMAR, Jayalaxmi;
APPLICANT: GRIFFIN, Jennifer A.; LI, Joana X.;
APPLICANT: YANG, Junming; THANGAVELU, Kavitha;
APPLICANT: BAUGHN, Mariah R.; BOROWSKY, Mark L.;
APPLICANT: YAO, Monique G.; CHAWLA, Naxinder K.;
APPLICANT: WASON, Patricia M.; GURURAJAN, Rajagopal;
APPLICANT: LEE, Sally; BECHA, Shanya D.;
APPLICANT: LEE, Soo Yeun; TRAN, Uyen K.;
APPLICANT: LEE, Soo Yeun; TRAN, Uyen K.;
APPLICANT: ELLIOTT, Vicki S.; LUO, Wen;
APPLICANT: LU, Yan; ZEBAROJADIAN, Yeganeh
TITLE OF INVENTION: PROTEIN MODIFICATION AND MAINTENANCE MOLECULES
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; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7632424CD1
US-10-480-988-8
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CURRENT FILING DATE: 2003-12-16
PRIOR APPLICATION NUMBER: PCT/US02/19360
PRIOR FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: US 60/300,508
PRIOR APPLICATION NUMBER: US 60/303,445
PRIOR APPLICATION NUMBER: US 60/303,445
PRIOR FILING DATE: 2001-07-06
PRIOR FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: US 60/305,405
PRIOR APPLICATION NUMBER: US 60/305,405
PRIOR APPLICATION NUMBER: US 60/305,405
PRIOR APPLICATION NUMBER: US 60/311,442
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-09
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SEQ ID NO 8
LENGTH: 414
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APPLICATION NUMBER: US 60/315,992
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THRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRALBILTNATQCTLLCPPPRLCTDNG 360
                                       PPLHHAKNCDFSFTGLQHVTDKIIMKKEKBEGIEKGQILSSAADIAATVQHTMACHLVKR 300
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WARREN, Bridget A.; ISON, Craig H.;
HONCHELL, Cynthia D.; NGUYEN, Danniel
LU, Dyung Aina M.; LEB, Ernestine A.;
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Sequence 2, Application US/10649273
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A 1
FILE REFERENCE: D0073 CNT
CURRENT APPLICATION NUMBER: US/10/649,273
CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-649-273-2
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PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
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                                                                                       THRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRALEILTNATQCTLLCPPPRLCTDNG 360
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                IMIAWNGIERLRAGLGILHDIEGIRYEPKCPLGVDISKEVGEASIKVPQLKMEI 414
                                                                     THRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRALBILTNATQCTLLCPPPRLCTDNG
                                                                                                                                          PPLHHAKNCDFSFTGLQHVTDKI IMKKEKEEGIEKGQILSSAADIAATVQHTMACHLVKR
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Sequence 2, Application US/10651722
GENERAL INFORMATION:
APPLICANT: BYSISTO: MYSIS SQUILD Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
FILE REFERENCE: D0073 DIV
CURRENT APPLICATION NUMBER: US/10/651,722
CURRENT FILING DATE: 2003-08-29

US-10-651-722-2

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Sequence 2, Application US/60266518
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A I
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: DO073 PSP
CURRENT APPLICATION NUMBER: US/60/266,518
CURRENT FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 28
SOPTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 414
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PRIOR FILING DATE: 2001-02-05
PRIOR PPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR PILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 2
LENGTH: 414
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; ORGANISM: Homo
US-10-651-722-2
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Best Local Sim:
Matches 414;
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Matches 414
                                                                                                          TYPE: PRT
ORGANISM: Homo
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Pred. No. 1.2e-214;
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Pred. No. 1.2e-214;
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GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
ITITLS OF INVENTION: POLYNUCLECTIDE ENCODING A PITTLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 PSPINAL CORD, MP-1
CURRENT APPLICATION NUMBER: US/60/282,814
CURRENT FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 414
TYPE: PAT
ORGANISM: Homo sapiens
US-60-282-814-2
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CURRENT APPLICATION NUMBER: US/60/495,114
CURRENT FILING DATE: 2003-08-15
NUMBER OF SEQ ID NOS: 91238
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1372
LENGTH: 425
TYPE: PRT
ORGANISM: Homo sapiens
US-60-495-114-1372
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US-60-495-114-1372
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US-10-918-754-1372
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CURRENT FILING DATE: 2004-08-16
NUMBER OF SEQ ID NOS: 91238
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1372
LENGTH: 425
                                                                                                                                                                               Sequence 1372, Application US/60495114
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METH
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL001480
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC
TITLE OF INVENTION: ENCODING HUMAN PROTEASE
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL001480
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Best Local :
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PROTEINS, METHODS OF DETECTION
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Sequence 19, Application PC/TUS0203353
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVEXTION: POLYNUCLEOTIDE ENCODING A 1
FILE REFERENCE: D0073 PCT
CURRENT APPLICATION NUMBER: PCT/US02/03353
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
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Best Local Similarity
Matches 414; Conserv
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                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOPTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: homo
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                                                121 ALSLGVGLSFSLQLVGQLKKPFIPIHHMEAHALTIRLTNKVEFPPLVLLISGGHCLLALV 180
121 ALSLGVGLSFSLQLVGQLKKPFIPIHHMEAHALTIRLTNKVEFPPLVLLISGGHCLLALV 180
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93.8%;
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Pred. No. 6e-211;
0; Mismatches 2;
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PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PATEENTIN VERSION 3.2
SEQ ID NO 19
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US-10-649-273-19
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GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Cómpany
TITLE OF INVENTION: POLYNUCLECTIDE ENCODING
FILE REFERENCE: D0073 CNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 98.4%;
Best Local Similarity 93.8%;
Matches 412; Conservative
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CURRENT FILING DATE: 2003-08-27
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                                                                  GQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNFYIRR 335
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                     ALBILTNATQCTLLCPPPRLCTDNGIMIAWNGIBRLRAGIGILHDIBGIRYEPKCPLGVD
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 ALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRGGLGILHDIEGIRYEPKCPLGVD
                                                                                                                                       PPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIFLISKVEQINIPGLCLKIAAHFCRYEK
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; SEQ ID NO 19
; LENGTH: 439
; TYPE: PRT
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US-10-651-722-19
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GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE,
FILE REPERENCE: D0073 DIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 412;
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Best Local Similarity 93.8%;
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PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/651,722
CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR FILING DATE: 2002-02-05
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                      ISKEVGEASIKVPQLKMBI 414
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ISKEVGEASIKVPQLKMEI 439
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; Sequence 19, Application US/60266518
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
; TITLE OF INVENTION: SPINAL CORD, MP-1

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US-60-266-518-19

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; FILE REFERENCE: D0073 PSP; CURRENT APPLICATION NUMBER: US/60/; CURRENT FILING DATE: 2001-02-05; NUMBER OF SEQ ID NOS: 28; SOFTWARE: Patentin version 3.0; SEQ ID NO 19; LENGTH: 439; TYPE: PRT ORGANISM: homo sapiens
US-60-266-518-19
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US-60-282-814-19
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GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILLE REFERENCE: D0073 PSP1
CURRENT APPLICATION NUMBER: US/60/282,814
CURRENT FILLNG DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.0
                                                                                                                                                                            SEQ ID NO 19
                                                           Matches
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Best Local Similarity 93.8%;
Matches 412; Conservative
                                                                                     Query Match
                                                                                                                                 LENGTH: 439
TYPE: PRT
ORGANISM: homo
                                                                       Local Similarity
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MLILIKTAGVFFKPSKRKVYEFLRSFNFHPETLFLHKIVLGIETSCDDTAAAVVDETGNV
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93.8%;
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                                                      Score 2090.5; DB Pred. No. 6e-211; 0; Mismatches
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Pred. No. 6e-211;
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APPLICANT: Leiby, Kevin R.
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Glucksmann, Maria A.
APPLICANT: Glucksmann, Maria A.
APPLICANT: Glucksmann, Maria A.
APPLICANT: Glucksmann, Maria A.
TITLE OF INVENTION: 14354 METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND USES
TITLE OF INVENTION: 14354 METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND USES
TITLE OF INVENTION: 14354 METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND USES
TITLE OF INVENTION: 14354 METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND USES
TURRENT APPLICATION NUMBER: US/10/012,140
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: 60/246,772
PRIOR APPLICATION NUMBER: 60/246,772
PRIOR APPLICATION NUMBER: 60/246,772
PRIOR APPLICATION NUMBER: 60/246,772
PRIOR APPLICATION NUMBER: 60/249,185
PRIOR TILING DATE: 2000-11-08
PRIOR TILING DATE: 2000-11-15
PRIOR TILING DATE: 2000-11-15
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LENGTH: 414
TYPB: PRT
ORGANISM: Homo sapiens
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                                                                                                                                           h 98.3%; Score 2088; DB 26;
Similarity 98.3%; Pred. No. 1e-210;
07; Conservative 3; Mismatches 4;
                                                                      LGEAIHSQTEVHLKTGGIVPPAAQQLHRENIQRIVQBALSASGVSPSDLSAIATTIKPGL 120
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В	Ş	<b>0</b>	Ş	Дb	Ş	Db	Q
361	361	301	301	241	241	181	181
361 IMIANNGIERLRAGLGILHDIEGIRYEPKCPLGVDISKEVGEASIKVPQLKMEI 414	361 IMIAWNGIERLRAGLGILHDIEGIRYEPKCPLGVDISKEVGEASIKVPQLKMEI 414	301 THRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRALBILTNATQCTLLCPPPRLCTDNG 360	301 THRAILECKORDLLPONNAVLVASGGVASNFYIRRALEILTNATOCTLLCPPPRLCTDNG 360	241 PPLHHAKNCDPSFTGLQHVTDKNNENRKQEBGIEKGQILSSAADIAATVQHTMACHLVKR 300	PPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMACHLVKR 300	181 QGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIK 240	181 QGVSDFLLIGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIK 240

Search completed: February 16, 2005, 13:18:55 Job time : 229.8 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/US11_NEW_COMB.pep:*

8: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
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217 STMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKG

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157 LTNKVBFFFLVLLISGGHÖLL            124 SVEPLEPPLLALLVSGGHTEL	Db 4 RYILAPETSCDETSVAVLKNDDBLLSNVIASQIESHKRPGGVVPENASRHHVEVITACIE  Qy 97 EALSASGYSESDLSALATTIKPGLALSLGVGLSPSLQLVGQLKKPFIPIHHMEAHALTIR	21.3%; Score 453; 34.2%; Pred. No. 1 /ative 57; Mismatch CDDTAAAVVDETGNVLGEAIHS	US-11-027-399-4857  US-11-027-399-4857; Sequence 4857, Application US/11027399; GENERAL INFORMATION:  APPLICANT: Doucette-Stamm, Lynn APPLICANT: Bush, David APPLICANT: Bush, David APPLICANT: Ceng, Qiandong APPLICANT: Houseweart, Chad Eric TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences; TITLE OF INVENTION: Number: US/11/027,399; CURRENT APPLICATION NUMBER: US/11/027,399; CURRENT APPLICATION NUMBER: US/04-0,833; PRIOR APPLICATION NUMBER: US 09/583,110 PRIOR APPLICATION NUMBER: US 09/583,110 PRIOR FILING DATE: 2000-05-26 PRIOR APPLICATION NUMBER: US 09/107,433 PRIOR FILING DATE: 1998-06-30 PRIOR APPLICATION NUMBER: US 60/085,131 PRIOR FILING DATE: 1998-05-12 PRIOR APPLICATION NUMBER: US 60/085,131 PRIOR FILING DATE: 1998-05-12 PRIOR APPLICATION NUMBER: US 60/085,131 PRIOR FILING DATE: 1997-07-02 NUMBER OF SEQ ID NOS: 5322 SEQ ID NO 4857 LENGTH: 336 TYPE: PRT ORGANISM: Streptococcus pneumoniae US-11-027-399-4857	ALIGNMENTS	26 103 4.8 848 6 US-10-436-715A-78 27 102 4.8 852 6 US-10-450-763-44045 28 101 4.8 917 6 US-10-805-075-2 29 101 4.8 917 6 US-10-805-075-4 30 98 4.6 398 8 US-60-643-717-274 31 98 4.6 398 8 US-60-643-717-274 32 97 4.6 1073 6 US-10-450-763-37549 33 97 4.6 1184 6 US-10-450-763-356201 34 96 4.5 612 7 US-11-027-893-5050 35 94.5 4.4 480 7 US-11-027-878-5050 36 94.5 4.4 480 7 US-11-027-878-5050 40 94.5 4.4 480 7 US-11-027-878-5050 41 94.5 4.4 480 7 US-11-027-877-5050 42 94.5 4.4 480 7 US-11-027-877-5050 43 94.5 4.4 480 7 US-11-027-877-5050 44 480 7 US-11-027-879-5050 45 94.5 4.4 480 7 US-11-027-879-5050 46 94.5 4.4 480 7 US-11-027-879-5050 47 94.5 4.4 480 7 US-11-027-879-5050 48 94.5 4.4 480 7 US-11-027-879-5050 49 94.5 4.4 480 7 US-11-027-879-5050 49 94.5 4.4 480 7 US-11-027-879-5050 41 94.5 4.4 480 7 US-11-027-879-5050 42 94.5 4.4 480 7 US-11-027-879-5050 43 94.5 4.4 480 7 US-11-027-879-5050
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CURRENT FILING DATE: 2004-12-30
PRIOR APPLICATION NUMBER: US 10/640,833
PRIOR FILING DATE: 2003-08-14
PRIOR APPLICATION NUMBER: US 09/583,110
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
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Best Local Similarity
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LENGTH: 336
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PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
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TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: 3687.1000-024
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                                                                L--AABITDVKVIIPPLRLCGDNAGMIAYASVSEWN
                                                                                                       LEILTNATQCTLLCPPPRLCTDNGIMIA-----WN 366
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APPLICANT: Zeng, Qiandong
APPLICANT: Opperman, Timothy
APPLICANT: Opperman, Timothy
APPLICANT: Houseweart, Chad Eric
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: 3687.1000-010
CURRENT APPLICATION NUMBER: US/11/028,169
CURRENT FILING DATE: 2004-12-30
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; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-11-027-878-4857
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Sequence 4857, Application US/11028169 GENERAL INFORMATION:
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LENGTH: 336
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CURRENT APPLICATION NUMBER: US/11/027,878
CURRENT FILING DATE: 2004-12-30
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PRIOR FILING DATE: 2003-08-14
PRIOR APPLICATION NUMBER: US 09/583,110
PRIOR FILING DATE: 2000-05-26
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                                                                                                                                           282 L--AAEITDVKVIIPPLRLCGDNAGMIAYASVSEWN 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 LTNKVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPEC
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                                                                                                                                                                                                                                                                              QILSSAADIAATVOHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRA
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                                                                                                                                                                                      LEILTNATQCTLLCPPPRLCTDNGIMIA-----
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Zeng, Qiandong
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34.2%; Pred. No. 1.2e-33;
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                                                                                                                                                                                           WN 366
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Bush, David

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APPLICANT: Department, Timothy
APPLICANT: Houseweart, Chad Eric
ITILE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
ITILE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
ITILE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
ITILE OF INVENTION PROMER: US(1)/028,204
CURRENT APPLICATION NUMBER: US(1)/028,204
CURRENT FILING DATE: 2004-12-30
PRIOR APPLICATION NUMBER: US(1)/640,833
PRIOR APPLICATION NUMBER: US(1)/640,833
PRIOR APPLICATION NUMBER: US(1)/640,833
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US(1)/640,833
PRIOR APPLICATION NUMBER: US(1)/640,833
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US(1)/640,833
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PRIOR APPLICATION NUMBER: US(1)/640
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PRIOR FILING DATE: 2003-08-14
PRIOR APPLICATION NUMBER: US 09/583,110
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 1998-05-20
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-05-30
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR FILING DATE: 1997-07-02
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SEQ ID NO 4857
LENGTH: 336
                                 NUMBER OF SEQ ID NOS:
SEQ ID NO 4857
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LENGTH: 336
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Zeng, Qiandong
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Pred. No. 1.2e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----EEYPVK--TLVVAGGVAANKGLRER 281
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US-11-027-877-4857
; Sequence 4857, Application US/11027877
; GENERAL INFORMATION:
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US-11-028-204-4857
                                                                                                                                                                                                                                                                                                    SEQ ID NO 4857
LENGTH: 336
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                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Zeng, Qiandong
APPLICANT: Opperman, Timothy
APPLICANT: Houseweart, Chad Eric
TITLE OP INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OP INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: 3687.1000-022
CURRENT APPLICATION NUMBER: US/11/027,877
CURRENT FILING DATE: 2004-12-30
PRIOR APPLICATION NUMBER: US 10/640,833
PRIOR APPLICATION NUMBER: US 09/583,110
PRIOR APPLICATION NUMBER: US 09/583,110
PRIOR APPLICATION NUMBER: US 09/583,110
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PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
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                                                                                                                                                               Local
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                                                                                                                                    21.3%; Score 453; DB 7; I al Similarity 34.2%; Pred. No. 1.2e-33; 115; Conservative 57; Mismatches 134;
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97 RALSASGVSPSDLSAIATTIKPGLALSLGVGLSFSLQLVGQLKKPPIPIHHMEAHALTIR 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 RYILAFETSCDETSVAVLKNDDELLSNVIASQIESHKRFGGVVPEVASRHHVEVITACIE
                                           L--AABITDVKVIIPPLRLCGDNAGMIAYASVSEWN 315
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FILE REFERENCE: 3687.1000-021

CURRENT APPLICATION NUMBER: US/11/027,879

CURRENT PILING DATE: 2004-12-30

PRIOR APPLICATION NUMBER: US 10/640,833

PRIOR PILING DATE: 2003-08-14

PRIOR APPLICATION NUMBER: US 09/583,110

PRIOR FILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/107,433

PRIOR PILING DATE: 1998-06-30

PRIOR APPLICATION NUMBER: US 60/085,131

PRIOR PILING DATE: 1998-05-12

PRIOR APPLICATION NUMBER: US 60/085,131

PRIOR PILING DATE: 1998-05-12

PRIOR PILING DATE: 1998-05-12

PRIOR PILING DATE: 1998-05-12

PRIOR PILING DATE: 1997-07-02

NUMBER OF SEQ ID NOS: 5322

SEQ ID NO 4857

LENGTH: 336

TYPE: PRT

ORGANISM: Streptococcus pneumoniae

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APPLICANT: Bush, David
APPLICANT: Zeng, Qiandong
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TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
                     277
                                                                                                                               124 SVEPLEPPLIALLVSGGHTELVYVSEAGDYKIVGETRDDAVGEAYDKVGRVMGL-----
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                                                                                                                                                                  157 LINKVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPEC
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                                                                                                                                                                                                                                                                                                                   37 KIVLGIETSCDDTAAAVVDETGNVLGEAJHSQTEVHLKTGGIVPPAAQQLHRENIQRIVQ 96
   QILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRA 336
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                                                        -TYPAGREIDELAHQGQDI-YDFPRAMIKEDNLEFSFSGLKSAFINLHHNAE-----QKG
                                                                                                                                                                                                                                            EALSASGVSPSDLSAIATTIKPGLALSLGVGLSFSLQLVGQLKKPFIPIHHMEAHALTIR 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L--AABITDVKVIIPPLRLCGDNAGMIAYASVSEWN 315
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Conservative
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34.2%; Pred. No. 1.2e-33;
tive 57; Mismatches 134; Indels
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                 US-11-027-802-4857

Sequence 4857, Application US/11027802

GENERAL IMPORMATION:

; APPLICANT: Doucette-Stamm, Lynn
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LENGTH: 336
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 Bush, David
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; TYPE: PRT ; ORGANISM: Streptococcus pneumoniae US-11-028-149-4857
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CURRENT FILING DATE: 2004-12-30
PRIOR APPLICATION NUMBER: US 10/640,833
PRIOR FILING DATE: 2003-08-14
PRIOR APPLICATION NUMBER: US 09/583,110
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR PILING DATE: 1998-05-12
PRIOR PILING DATE: 1998-05-12
PRIOR FILING DATE: 1997-07-02
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 5322
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                                                                                                                                                                                                                                                                                                                                                                                          124 SVEPLEPPLIALLVSGGHTELVYVSEAGDYKIVGETRDDAVGEAYDKVGRVMGL-----
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L--AABITDVKVIIPPLRLCGDNAGMIAYASVSEWN
                                                            LEILTNATQCTLLCPPPRLCTDNGIMIA-----WN 366
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                                                                                                                                                                                                                                                         -TYPAGREIDELAHOGODI-YDFPRAMIKEDNLEFSFSGLKSAFINLHHNAE-----QKG
                                                                                                                                ESLST-EDLCASFOAAVMDILMAKTKKAL-----EBYPVK--TLVVAGGVAANKGLRER
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Opperman, Timothy
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US-11-07-890-4857

(Sequence 4857, Application US/11027890)

(SERRAL INFORMATION:

APPLICANT: Doucette-Stamm, Lynn

APPLICANT: Bush, David

APPLICANT: Bush, David

APPLICANT: Opperman, Timothy

APPLICANT: Houseweart, Chad Bric

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

FILE REFERENCE: 3687.1000-020

CURRENT APPLICATION NUMBER: US/11/027,890

CURRENT FILING DATE: 2004-12-30

PRIOR APPLICATION NUMBER: US 10/640,833

PRIOR APPLICATION NUMBER: US 09/583,110

PRIOR APPLICATION NUMBER: US 09/583,110
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SEQ ID NO 4857
LENGTH: 336
TYPE: PRT
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TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: 3687.1000-011
CURRENT APPLICATION NUMBER: US/11/027,802
CURRENT FILING DATE: 2004-12-30
PRIOR APPLICATION NUMBER: US 10/640,833
PRIOR FILING DATE: 2003-08-14
PRIOR APPLICATION NUMBER: US 09/583,110
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1997-07-02
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APPLICATION NUMBER: US 09/107,433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 EALSASGVSPSDLSAIATTIKPGLALSLGVGLSFSLQLVGQLKKPFIPIHHMEAHALTIR 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L--AAEITDVKVIIPPLRLCGDNAGMIAYASVSEWN 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 453; DB 7;
Pred. No. 1.2e-33;
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; PRIOR FILING DATE: 1998-06-30; PRIOR APPLICATION NUMBER: US 60/085,131; PRIOR FILING DATE: 1998-05-12; PRIOR APPLICATION NUMBER: US 60/051,553; PRIOR FILING DATE: 1997-07-02; NUMBER OF SEQ ID NOS: 5322; SEQ ID NO 4857; LENGTH: 336
; TYPE: PRT; ORGANISM: Streptococcus US-11-027-892-4857
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                                                                                                                 CURRENT APPLICATION NUMBER: US/11/027,892
CURRENT FILING DATE: 2004-12-30
PRIOR APPLICATION NUMBER: US 10/640,833
PRIOR FILING DATE: 2003-08-14
PRIOR APPLICATION NUMBER: US 09/583,110
PRIOR APPLICATION NUMBER: US 09/583,110
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR PILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR PILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
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US-11-027-892-4857
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                                                                   SEQ ID NO 4857
LENGTH: 336
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APPLICANT:
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Opperman, Timothy
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34.2%; Pred. No. 1.2e-33;
ative 57; Mismatches 134;
                       pneumoniae
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Query Match

21.3%;

Score 453;

DB 7;

Length 336;

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Best Local Similarity
Matches 115; Conserv
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SEQ ID NO 4857
LENGTH: 336
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APPLICANT: Houseweart, Chad Eric
APPLICANT: Houseweart, Chad Eric
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: 3687.1000-019
FILE REFERENCE: 3687.1000-019
CURRENT APPLICATION NUMBER: US 10/640,899
CURRENT FILING DATE: 2003-08-14
PRIOR APPLICATION NUMBER: US 09/583,110
PRIOR FILING DATE: 2003-08-14
PRIOR APPLICATION NUMBER: US 09/583,110
PRIOR APPLICATION NUMBER: US 09/583,110
PRIOR APPLICATION NUMBER: US 09/583,110
PRIOR APPLICATION NUMBER: US 09/583,110
PRIOR APPLICATION NUMBER: US 09/583,110
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ORGANISM: Streptococcus pneumoniae
-11-028-099-4857
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231
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                                                                                                                        97 EALSASGVSPSDLSAIATTIKPGLALSLGVGLSFSLQLVGQLKKPFIPIHHMEAHALTIR 156
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                                                                       EALAEAGITEEDVTAVAVTYGPGLVGALLVGLSAAKAFAWAHGLPLIPVNHMAGHLMAAQ
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Opperman, Timothy
                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                    21.3%; Score 453; DB 7; Length 336; 34.2%; Pred. No. 1.2e-33;
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                                                                                                                                                                                                                                                                             57; Mismatches 134; Indels
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TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: 3687.1000-007
CURRENT PAPLICATION NUMBER: US/11/028,197
CURRENT FILING DATE: 2004-12-30
PRIOR APPLICATION NUMBER: US 10/640,833
PRIOR FILING DATE: 2003-08-14
PRIOR APPLICATION NUMBER: US 09/583,110
PRIOR RPILING DATE: 2000-05-26
PRIOR RPILING DATE: 1998-05-20
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR PILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR RPILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR PILING DATE: 1998-06-30
PRIOR PILING DATE: 1998-06-07
PRIOR PILING DATE: 1998-05-12
PRIOR RPILING DATE: 1998-05-12
PRIOR RPILING DATE: 1998-05-12
PRIOR PILING DATE: 1998-05-12
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Best Local (
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APPLICANT:
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     282
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                                                                                                                                QILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRA 336
                                                                                                                                                                                                     -TYPAGREIDELAHQGQDI-YDFPRAMIKEDNLEFSFSGLKSAFINLHHNAE-----QKG
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     L--AAEITDVKVIIPPLRLCGDNAGMIAYASVSEWN
                                                   LEILTNATQCTLLCPPPRLCTDNGIMIA-----WN
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Opperman, Timothy
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34.2%; Pred. No. 1.2e-33;
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281

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US-11-028-050-4857; Sequence 4857, Application US/11028050; GENERAL INFORMATION:
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SEQ ID NO 4857
LENGTH: 336
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GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Houseweart, Chad Eric
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
TITLE OF INVENTION: US/11/027,844
CURRENT APPLICATION NUMBER: US/11/027,844
CURRENT FILING DATE: 2004-12-30
PRIOR APPLICATION NUMBER: US 10/640,833
PRIOR APPLICATION NUMBER: US 10/540,833
PRIOR APPLICATION NUMBER: US 09/583,110
APPLICANT: Houseweart, Chad Eric
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
                                                                          APPLICANT: Doucette-Stamm, Lyr
APPLICANT: Bush, David
APPLICANT: Zeng, Qiandong
APPLICANT: Opperman, Timothy
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PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
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APPLICANT: Bush, David
APPLICANT: Zeng, Qiandong
APPLICANT: Opperman, Timothy
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PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR FILING DATE: 1997-07-02
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34.2%; Pred. No. 1.2e-33;
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CURRENT APPLICATION NUMBER: US/11/028,050
CURRENT FILING DATE: 2004-12-30
PRIOR APPLICATION NUMBER: US 10/640,833
PRIOR PILING DATE: 2003-08-14
PRIOR PILING DATE: 2003-08-14
PRIOR APPLICATION NUMBER: US 09/583,110
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR PILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR PILING DATE: 1997-07-02
PRIOR PILING DATE: 1997-07-02
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SEQ ID NO 4857
LENGTH: 336
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Best Local
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                                                                                                                                                             277
282
                                                 337 LEILTNATQCTLLCPPPRLCTDNGIMIA-----WN 366
                                                                                                        231 ESLST-EDLCASFQAAVMDILMAKTKKAL-----EEYPVK--TLVVAGGVAANKGLRER 281
                                                                                                                                                                                                                 178
                                                                                                                                                                                                                                                                                                                       124 SVEPLEFPLLALLVSGGHTELVYVSEAGDYKIVGETRDDAVGEAYDKVGRVMGL-----
                                                                                                                                                                                                                                                                                                                                                                                                                        37 KIVLGIETSCDDTAAAVVDETGNVLGEAIHSQTEVHLKTGGIVPPAAQQLHRENIQRIVQ 96
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L--AAEITDVKVIIPPLRLCGDNAGMIAYASVSEWN
                                                                                                                                                       QILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRA 336
                                                                                                                                                                                                                                          STMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKG
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177

216

230 276

Search completed: February 16, 2005, 13:19:29 Job time : 15.15 secs

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -MODEL=frame+_p2n.model -DEV=x1h
-Q=/Cg12 1/USPTO_spool/US1649273/runat_14022005_114702_16399/app_query.fasta_1.1429
-Q=/Cgn2 1/USPTO_spool/US1649273/runat_14022005_114702_16399/app_query.fasta_1.1429
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MTNMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bite -START=1 -END=-1 -MAYRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pco -NORN=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10649273 _GCGN 1 _8655 _Grunat _14022005_114702_16399 -NCPU=6 -ICPU=3
-NO_MMAP _LARGEQUERY -NEG _SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV _TIMEOUT=120 -WARN _TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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  2090.5
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  100.0
100.0
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2125
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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EC011904
AR428803
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BC011904 Homo sapi
AR428803 Sequence
AR428808 Sequence
AJ295148 Homo sapi
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AL591792 Sinorhizo	5917	_	333800		568.5	\$
Wolbachi	17258	-	260271	•	7	44
tinu	06501	N	110000	•	819	43
Sequenc	AX874913	σ	571	•	N	42
Primer	BD154975	σ	571	•	629	41
12	AK070912	œ	1672	•	656	40
4577		œ	1557	•	52	39
64	AY063864	œ	1567	•	39	38
	AY117283	œ	1474	31.5	39	37
024338	w	œ	1443	•	39	36
Brosophi	0351	ω	0743	•	87	35
71 Drosophi	AC010671	w	026	•	687.5	34
~	AC018262	N	14679	32.4	83	ű
Sequence	CQ606431	9	3656	•	687.5	32
٠ı	AK027836	9	1385	•	•	
9 Sequence	AX878239	σ	1385	33.0	700.5	30
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7 Zebraí	AL672217	v	117322	33.4	709	28
	AK113378	ω	1474	33.4	710	27
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~	AY051882	w	1576	•	714.5	25
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	BX93096	თ	1558	•	1208	15
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2 Mus	BCC	10	1844	•	8	ø
	AK055441	9	2208	91.5	1944	œ
	1371	σ	2208	•	1944	7
	AX664695	σ	1820	98.3	8	σ
-	469	σ	1245	98.3	2088	u

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## ALIGNMENTS

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RESULT 1
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BC011904
Homo sapiens O-sialoglycoprotein endopeptidase-like 1, mRNA (cDNA clone MGC:20293 IMAGE:4121450), complete cds.

BC011904
VERSION
BC011904.2 GI:40225818
KEYWORDS
SOURCE
Homo sapiens (human)
BC011904.2 GI:40225818
BC011905.3 HAGE:4121450), complete cds.

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Alignment Scores:
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AUTHORS
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JOURNAL
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NIH-MGC Project URL: http://mgc.nci.nih.gov
On Dec 19, 2003 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (30-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.B., Jones,S.J. and Marra,M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 28 Row: i Column: 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Alele,K., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Gupta,J., Haghighi,P.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,B., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg, R.
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RALEILTNATQCTLLCPPFRLCTNGINIAMNGIERLRAGLGILHDIEGIRYEFKCFL
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Location/Qualifiers
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                                               ThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaVal 320
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                          ACACATCGGGCTATTCTGTTTTGTAAGCAGAGACTTGTTTACCTCAAAATAATGCAGTA
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RESULT 3 AR428808 LOCUS AR428808 AR428808 AR428808 AREPINITION ACCESSION AR428808 VERSION AR428808 AR428808 AR428808 AR428808 AR428808  VERSION AR428808 AR428808 AR428808 AR428808 AR428808 ARA428808 AR428808 AR42808 AR428808 AR4		1251 ACAAACGCAACACAGTGCACTTTGTTGTGTCCTCCCAGACTATGCACTGATAATGGC  361 IleMetIleAlaTtpAsnGlyIleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAsp	301 1131 321 1191	261 ABPLYSIIeIleMetLYBLYSGluLYSGluGluGlYIleGluLYSGlYGlnIIeLeuSer	Oy 221 GlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPheHisPheAspIleLys 240	Qy 181 GlnGlyValSerAspPheLeuLeuGlyLysSerLeuAspIleAlaProGlyAspMet 200	Qy 121 AlaLeuSerLeuGlyValGlyLeuSerPheSerLeuGlnLeuValGlyGlnLeuLysLys 140

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                                                                                                       GlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPheHisPheAspIleLys
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GATAAAATAATAATGAAAAAGGAAAAAGAGGGAAGGTATATTTCTAATTAGTAAAGTTGAA
                                              CCTCCCTTGCATCATGCTAAAAATTGTGATTTTTCTTTTACTGGACTTCAACACGTTACT
                                                                                           GGTGGGAAAGCCATAGAGCATTTGGCCAAACAAGGAAATAGATTTCATTTTGACATCAAA
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Homo sapiens mRNA for putative s
AJ295148
AJ295148.1 GI:11071726
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                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (27-OCT-2000) Chen J.M.,
Laboratory, The Babraham Institute,
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                                        ASPLYSIleIleMetLysLysGluLysGluGluGlyIle------
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IERLRGGLGILHDIEGIRYEPKCPLGVDISKEVGEASIKVPQLKMEI"
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Sequence 6 from Patent WO02074960.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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## Alignment Scores: Pred. No.: 2088.00 Score: 2088.00 Matches: 407 Percent Similarity: 99.03\$ Best Local Similarity: 98.26\$ Cuery Match: 6 Cuery Match: 6 Caps: 0 US-10-649-273-2 (1-414) x AX664695 (1-1820) Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation: 0 Outlief Courty Nation

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                   Homo sapiens (human)
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Masuho,Y.

Full-length cDNAs

Full-length cDNAs

Fatent: EP 1293569-A 400 19-MAF

Helix Research Institute (JP)

Biotechnology (JP)

Location/Qualifiers
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Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
GlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPheHisPheAspIleLys 240
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Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sebine, M., Obayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Nagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Shiratori, A., Sudo, H., Marada, K., Yokoi, T., Furuya, T., Kikkawa, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hiraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Moriya, S., Moniyama, H., Satoh, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Pukuzumi, Y., Fujimori, Y., Komiyama, M., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Cashi, K., Hita, M., Itakura, S., Pukuzumi, Y., Fujimori, Y., Kowakami, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Kobatake, N., Inagaki, H., Shigeta, K., Senba, T., Matsumura, K.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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2208 bp mRNA linear PRI 30-JAN-2004
sapiens cDNA FLJ30879 fis, clone FEBRA2004592, highly similar
mno sapiens mRNA for putative sialoglycoprotease type 2.
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Direct Submission

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Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

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Economy, Trade and Industry of Japan; cDNA full insert sequencing:

Research Association for Biotechnology (RAB); cDNA library

construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

Byaluation; clone selection for full insert sequencing: RAB and
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Matches:
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                                                                                                                                                                                                                                                                                                                 ThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaVal 320
                                                                                                                                                                                                                                                                                                                                                                                     SerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCysHisLeuValLysArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTGACAAGGTGGCAAGAAGACTTCCTTTAATAAAACATCCAGAGTGCTCCACCATGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGluCysSerThrMetSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlnGlyValSerAspPheLeuLeuLeuGlyLysSerLeuAspIleAlaProGlyAspMet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AlaLeuSerLeuGlyValGlyLeuSerPheSerLeuGlnLeuValGlyGlnLeuLysLys
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                                                                                            IleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAsp
||||||||
                                                                                                                                                                                                                                         LeuValAlaSerGlyGlyValAlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeu
                                                                                                                                                                                                                                                                                          ACACATCGGGCTATTCTGTTTTGTAAGCAGAGAGACTTGTTACCTCAAAATAATGCAGTA 1303
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                                                                                                                                                                                                                     CIGGTIGCATCIGGIGGIGICGCAAGIAACITCIGTATCCGCAGAGCICIGGAAATTITA 1363
                                                                                                                                                                                                                                                                                                                                                                    TCAGCAGCAGACATTGCTGCCACAGTACAGCACACAATGGCATGTCATCTTGTGAAAAGA
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-TGATGTCCTCTTGGAGTAGACATATCAAAAGAAGTT 1471
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

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Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consorcium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 123 Row: d Column: 22
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 2131240 Location/Qualifiers
                                                                                                                                                                                                                                                   web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Bengamin,B.,
Akhter,N., Ayele,K., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Gupta,J., Haghighi,P.,
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Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,B.D.
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Submitted (15-SEP-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Tissue Procurement: Gilbert !
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Contact: MGC help desk
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                     GCCCTAAGCTTAGGAGTCGGCTTATCCTTTAGCTTACAGCTAGTAAAATCGGTTTAAAAAG
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333. .1397
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possible chaperone activity [Posttranslational
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QILSSAADIAAAVQHATACHLAKRTHRAILFCKQKNLLSPANAVLVVSGGVASNLYIR
KALEIVANATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGVLHDVEDIRYEPKCPL
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SCDDTGAAVVDETGNVLGEALHSQTQVHLKTGGIVPPVAQDLHRENIQRIVEETLSAS
RITPSDLSAIATTIKPGLALSLGVGLSFSLQLVNRFKXPFIPHHMEAHALTIRLTNK
VEPPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECST
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/db_xref="CDD:COG0533"
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/product="Unknown (protein
/protein_id="AAH58172.1"
/db_xref="GI:34849664"
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/clone="MGC:67870 IMAGE:5012054"
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/strain="CZECH II"
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Sequence 17
AR541929
AR541929.1
                                                                           1 (bases 1 to 1416)
Tang,Y.T., Zhou,P., Goodrich,R., Liu,C.,
Zhang,J., Zhao,Q.A., Yang,Y., Xue,A.J., V
Wang,D. and Drmanac,R.T.
                                      Nucleic acids and polypeptides
Patent: US 6743619-A 177 01-JUN-2004;
Location/Qualifiers
                                                                                                                                              Unknown.
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/organism="unknown"
/mol_type="genomic DNA"
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IleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAsp 380
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                                                                                                                                                                                                    AlaCysHisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeu 313
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                         ArgLeuCysThrAspAsnGlyIleMetIleAlaTrpAsnGlyIleGluArgLeuArgAla 373
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                                                                                                                                                                                                                                                                                          ACTGGACTTCAACACGTTACTGATAAAATAATAATGAAAAAGGGAAAAAGGGAAGGTATT
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malak, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Halton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Direct Submission

Submitted (02-AUG-2004) National Institutes of Health, Mammalian Submitted (02-AUG-2004) Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                  cDNA Library Preparation: Express Genomics (LLNL) cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford, web site:

http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus cDNA clone
BC078974
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Scrice: IRAK Flate: 182 Row: f Column: 6 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Howard Jacobs
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GlnGlyValSerAspPheLeuLeuLeuGlyLysSerLeuAspIleAlaProGlyAspMet
                                                                  ValGluPheProPheLeuValLeuLeuIleSerGlyGlyHisCysLeuLeuAlaLeuVal 180
                                                                                                                ProPheIleProIleHisHisMetGluAlaHisAlaLeuThrIleArgLeuThrAsnLys
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Sequence 23 from patent
AR428809
AR428809.1 GI:40188595
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Chen, J., Feder, J.N., Nelson, T.C., Krystek, S.R. and Duclos, Polynucleotides encoding a novel metalloprotease, MP-1 Patent: US 6642041-A 23 04-NOV-2003;
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1 (bases 1 to 1522)
Boardman, P. B., Bonfield, J.K., Brown, W.R.A., Carder, C., Chalk Croning, M.D.R., Davies, R. H., Francis, M.D., Grafham, D.V., Hubbard, S.J., Humphray, S.J., Hunt, P.J., Maddison, M., McLaren Niblett, D., Overton, I.M., Rogers, J., Scott, C.B., Taylor, R.G. Tickle, C. and Wilson, S.A.
                                                                                                                                            Gallus gallus (chicken)
Gallus gallus
                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallins.
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Submitted (02-FEB-2004) Sanger Institute, Hinxton, Cambridgeshire,
Submitted (102-FEB-2004) Sanger Institute, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: chickest@bms.umist.ac.uk
CB10 1SA, UK. E-mail enquiries: chickest@bms.umist.ac.uk
CB10 1SA, UK. E-mail enquiries: chickest@bms.umist.ac.uk
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This sequence is from the
                 SerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPheHis
|||:::||||||||||||||||||||||||::: |||:::
CACGGCATGGCTGGGGGAAGGCAATAGAGCACCTGGCTCAAACCGGAGACTGGCAACAG
                                                                                                                                                                                                        ProGlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGluCys
                                                                                                                                          GlnLeuLysLysProPheIleProIleHisHisMetGluAlaHisAlaLeuThrIleArg
                                                                                                                                                                                                                                                                                                                                                      LysProGlyLeuAlaLeuSerLeuGlyValGlyLeuSerPheSerLeuGlnLeuValGly 136
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/mol type="mRNA"
/strain="Layer and broiler"
/db xref="taxon:9031"
/clone="ChEST189114"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="CSEQRBN11"
/dev_stage="adult"
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                                                                                                                   TITLE
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Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
P. 20188257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BC038910 1017 bp mRNA linear Mus musculus O-sialoglycoprotein endopeptidase-like clone IMAGE:5053559), partial cds.
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      (bases 1 to 1017)
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                62
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Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (25-OCT-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution through the I.M.A.G.E. Consortium/LLNL at: Series: IRAK Plate: 86 Row: f Column: 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg, R.
                                LysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGlyLeuGlnHisVal
                                                                                                                   SerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPheHisPheAspIle
                                                                                                                                                                                                          MetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGluCysSerThrMet
                                                                                                                                                                                                                                                                                                  ValGlnGlyValSerAspPheLeuLeuLeuGlyLysSerLeuAspIleAlaProGlyAsp
                                                                                                                                                                                                                                                                                                                                                                AAAGTAGAATTTCCTTTTTTAGTTCTTTTGATTTCTGGCGGTCACTGCCTGTTGGCATTA
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    ATGCTTGACAAGGTGGCAAGAAGACTTTCTTTAATCAAACATCCAGAATGTTCTACAATG
                                                                                                                                                                                                                                                                        GTCCAAGGTGTTTCCGATTTCCTGCTCCTTGGGAAGTCTTTGGACATAGCACCAGGCGAC
                                                                                            AGTGGTGGAAAAGCTATAGAACAGTTGGCCAAAGACGGAAATAGATTCCATTTTACTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Liver, normal.
/clone_lib="NCI_CGAP_Li9"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="IMAGE:5053559"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="FVB/N"
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Boardman, P.B., Bonfield, J.K., Brown, W.R.A., Carder, C., Chalk Croning, M.D.R., Davies, R.M., Francis, M.D., Gratham, D.V., Hubbard, S.J., Humphray, S.J., Hunt, P.J., Maddison, M., McLaren Niblett, D., Overton, I.M., Rogers, J., Scott, C.B., Taylor, R.G. Tickle, C. and Wilson, S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BX930963
Gallus gallus finished (
BX930963
BX930963.2 GI:46016890
                                                                                                                                                                                                                                          Submitted (29-MAR-2004) Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: chickest@bms.umist.ac.uk On Apr 1, 2004 this sequence version replaced gi:41631491. BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (chicken)
Gallus gallus
                                                                                                                             and poly A-trimmed. EcoRI-NotI cut cDNA was then ligated into the vector. Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI Host: Escherichia coli DH10B.
                                                                                                                                                                   BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST cDNA from a library constructed by Elizabeth Bosch. cDNA from RNA extracted from limbs,
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; VerteBrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                 sequencing project.
This sequence is from the
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              /organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/dh_xref="taxon:9331"
/clone="ChES7727n16"
/clone_lib="CSEQCHL20"
                                                                                                                 Location/Qualifiers
 dev_stage="stage 36"
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                            ArgieüCysThrāspāunGlyIlemetileAlaTrpAsnGlyIleGluArgLeuArgAla 373
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AGGCTGTGCACCGATAATGGTGTTATGATTGCATGGAATGGCATTGAAAGGTTGCGTGCA 138
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                                                                                    AGAAAAGGACTGCAGACTCTGGCAAATGCAAACGGTTTTGCTTTTCTGTCTCCTCCA
                                                                                                              ArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProPro
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Search completed: February 16, 2005, 18:02:36 Job time : 6632 secs	394 ValAspIleSerLysGluValGlyGluAlaSerIleLysValProGlnLeuLys 411	::: 1386 GGATGTGGTATTTTATACAGTACTGATGGCATCCGCTATGAACCAAAAGCTCCCCTTGGA 1445

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Result
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-Q=/Cgn2 1/USPTO_spool/US16649273/runat_14022005 114702 16389/app_query.fasta_1.1429
-DB=N_Geneseq_16Dec04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -RND=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10649273 @CGN 1 1057 @runat 14022005 114702 16389 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WANN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPDXT=0.5 -FGAPOP=6
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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Abt23207 Human pro
Aad46856 Human gly
Aca60887 Human cDN
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Continuation (46 o	) ACF67367_45	ĭ	110000	22.2	472.5	45	
Acf71364 Photorhab		ï	1014	22.2	472.5	44	
Ach96255 Klebsiell		11	1032	22.3	474.5	43	
Continuation (6 of	AAT42063	N	110000	22.4	•	42	ი
Aca34150 Prokaryot	ACA34150	8	1029	22.4	475.5	41	
	AAS53309	4.	1029	22.4	475.5	40	
Aaq27645 Glycoprot	AAQ27645	N	1315	22.5	479	39	
	Þ	4	1014	22.7	•	38	
56		10	1074	22.7	•	37	
Aca44384 Prokaryot	ACA44384	8	1020	22.7	482.5	36	
7	ACA54107	œ	1014	22.8	483.5	35	
Aca32641 Prokaryot	ACA32641	œ	1014	•	٠.	ų 4	
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	) ADG73343	5	1026	•	•	31	
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73341		10	1026	•	?	29	
Pro	ACA42146	œ	1026	•	492.5	28	
	AAS54064	4	1026	23.2	492.5	27	
Aca43173 Prokaryot	ACA43173	œ	1032	23.3	494.5	26	
~		11	1206	23.5	499.5	25	
Abq90383 M. capsul	ABQ90383	σ	1092	•	500	24	
0		12	1053	23.6	501	23	
	AAF28551	4	94750	23.6	502	22	
	ACA39102	œ	1044	23.6	502	21	
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Aad48239 Ehrlichia	AAD48239	σ	4360	25.0	531.5	19	
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w	AAH12983	4	571	•	629	17	
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	ABL24632	4	3656	•	687.5	15	ი
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4633 Drosophi	ABL24633		1601	٠	714.5	13	
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## ALIGNMENTS

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RESULT 1
ABA93268
ABA93268 standard; cDNA; 2058 BP.

XX
AC ABA93268;
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AC ABA93268;
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I9-APR-2002 (first entry)
XX
Human O-sialoglycoproteinase-like protein encoding cDNA SEQ ID NO:1.
XX
KW Human; O-sialoglycoproteinase-like protein; OSGPLP; enzyme; gene; ss.
XX
Homo sapiens.
XX
FT CDS
FH Key
CDS
I10..1354
FT /*tag= a
FT /*rtag= a
FT /*product= "O-sialoglycoproteinase-like proteinse-like protein"
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PD 24-OCT-2001.
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PP 19-APR-2000; 2000CN-00106834.
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PR 19-APR-2000; 2000CN-00106834.
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PA (SHAM-) SHANGHAI SHENGYUAN GENE DEV CO LTD.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O-sialogycoproteinase-like protein and encoding polynucleotide, useful for diagnosing, preventing and treating related diseases.
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                                            GlnGlyValSerAspPheLeuLeuLeuGlyLysSerLeuAspIleAlaProGlyAspMet
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LeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGluCysSerThrMetSer
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05-FEB-2001; 2001US-0266518P 05-FEB-2002; 2002WO-US003353 WO200272751-A2 Homo sapiens.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes an isolated nucleic acid molecule (I) encoding a metalloprotease (MP-1). (I) is useful for preventing, treating, or ameliorating a medical condition, particularly an immune disorder, an aberrant glutemate transport or motor neuron disorder, such as a myotrophic lateral sclerosis (ALS), its juvenile form or an ALS-like condition. The compositions and methods are also useful for diagnosing, prognosticating, treating, ameliorating and/or treating disorders associated with MP-1 activity, e.g. diabetes, cancer, reproductive associated with MP-1 activity, e.g. diabetes, cancer, reproductive cor Cushing's syndrome, neurodegenerative diseases (Alzheimer's disease, Parkinson's disease, huntington's disease or Tourette syndrome), liver and renal diseases and immune disorders (e.g. Alzheimer's disease, pulmonary diseases (e.g. AlDS, rheumatoid arthritis or sepsis), pulmonary diseases (e.g. Dremonita, emphysema or cystic fibrosis) and vascular, inflammatory and neurological disorders (e.g. Alzheimer's disease or Parkinson's disease). This sequence represents a metalloprotease MPI polynucleotide
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autoimmune;

cerebroprotective; antiparkinsonian; nootropic; antinflammatory; antiparetrial; synaecological; antibacterial; virucide; protozoacide; antiparasitic; cell proliferative disease; pMOD; protein modification and maintenance molecule; immunogenic fragment;

inflammatory disease; neurological disorder;

Cytostatic; antiarteriosclerotic; anti-HIV; antiallergic; anticonvolsant; Human protein modification + maintenance molecule DNA SEQ ID No 36. 01-MAY-2003 ABT23207; **ABT23207** 

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Percent Similarity:
Best Local Similarity:
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06-JUL-2001; 2001US-0303445P.
13-JUL-2001; 2001US-0305405P.
09-AUG-2001; 2001US-0311442P.
24-AUG-2001; 2001US-0314821P.
29-AUG-2001; 2001US-0315992P.
03-MAY-2002; 2002US-0378205P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gastrointestinal; developmental; vesicle trafficking disorder; infection;
protein-protein interaction; drug-target interaction;
gene expression profile; human; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated human PMOD polypeptide and polynucleotide, useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant PMOD expression, e.g. cancer, AIDS, atherosclerosis
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ThrAsnAlaThrGlnCysThrLeuLeuCysProProProArgLeuCysThrAspAsnGly
                                                                                                                                   SerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCysHisLeuValLysArg
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                                          LeuValAlaSerGlyGlyValAlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeu
                                                                           ThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaVal
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The present invention relates to novel 38650, 28472, 5495, 65507, 81588 or 14354 nucleic acid molecules which encode adenosine deaminase, glycoprotease or seven transmembrane domain (?TM) receptor family members. Sequences of the invention are useful in diagnosing and treating cancer or aberrant cellular proliferation and/or differentiation (e.g. colon or lung cancer), immune disorders (e.g. selective IgA deficiency, rheumatoid
                                                                                                                                                                                                                                                                                New 38650, 28472, 5495, 65507, 81588 or 14354 nucleic acid molecules, useful for diagnosing and treating cancer, immune, cardiovascular, hematopoietic, brain, pain, metabolic, liver or platelet disorders, a
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08-NOV-2000; 2000US-0246772P.
15-NOV-2000; 2000US-0249185P.
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Alignment

Sequence 1820 BP; 543 A; 365 C;

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518 T; 0 U; 1 Other;

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The invention relates to an isolated 38650 (encoding adenosine CC deaminase), 28472 (encoding a glycoprotease), 5495 (encoding a 7 CC transmembrane receptor), 65507, 81588 or 14354 nucleic acid molecule (or CC a sequence which is at least 60% identical to the six nucleic acids or CC their open reading frames, fragments of at least 15 nucleotides, CC naturally occurring variants, or a DNA insert of the plasmid deposited CC with the American Type Culture Collection as Accession No. not defined in CC the specification, which encodes the amino acid sequence). Also included are a host cell containing the nucleic acids (used to produce the protections) the encoded proteins, an antibody that selectively binds to CC the polypeptide, and identifying a compound that binds to/modulates the CC activity of the polypeptide. The nucleic acid molecules, polypeptides and CC methods are useful for diagnosing, treating cancer, aberrant cellular CC proliferation and/or differentiation, immune disorders, heart disorders, CC haematopoeitic disorders, blood vessel disorders, brain disorders, pain CC and metabolic disorders, liver disorders and platelet disorders (many ceamples of these disorders are given in the specification). The present cc sequence is the Human CDNA 28472 encoding a glycoprotease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated 38650, 28472, 5495, 65507, 81588 and 14354 nucleic acid molecules, useful for diagnosing, treating cancer, pain, or immune, heart, endothelial cell, hematopoeitic, blood vessel, brain, metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2;
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Percent Similarity:
Best Local Similarity:
Query Match:
DB: ð 밁 δ 밁 S 문 Ś US-10-649-273-2 (1-414) x ACA60887 (1-1820) No.: 266 206 13 41 21 GluPheLeuArgSerPheAsnPheHisProGlyThrLeuPheLeuHisLysIleValLeu GlyIleGluThrSerCysAspAspThrAlaAlaAlaValValAspGluThrGlyAsnVal GAATTTTTAAGAAGTTTTAATTTTCATCCTGGAACACTATTTCTTCATAAAATAGTATTG LeuGlyGluAlaIleHisSerGlnThrGluValHisLeuLysThrGlyGlyIleValPro 80 GGAATTGAAACTAGTTGTGATGATACAGCAGCTGCTGTGGTGGATGAAACTGGAAATGTG 1.24e-208 2088.00 99.03% 98.31% 98.26% Conservative: Mismatches: Indels: Length: Matches: Gaps: 1820 407 3 0

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AlaLeuSerLeuGlyValGlyLeuSerPheSerLeuGlnLeuValGlyGlnLeuLysLys 140

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AlaSerGlyValSerProSerAspLeuSerAlaIleAlaThrThrIleLysProGlyLeu

ProAlaAlaGlnGlnLeuHisArgGluAsnIleGlnArgIleValGlnGluAlaLeuSer 100

TTGGGAGAAGCAATACATTCCCAAACTGAAGTTCATTTAAAAACAGGTGGGATTGTTCCT

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CCAGCAGCTCAACAGCTTCACAGAGAAAATATTCAACGAATAGTACAAGAAGCTCTTTCT

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                       Cancer; aberrant cell proliferation; aberrant cell differentiation; breast cancer; ovarian cancer; prostate cancer; colon cancer; lung cancer; immune disorder; heart disorder; cardiovascular disorder; endothelial disorder; hematopoietic disorder; blood vessel disorder; brain disorder; pain; metabolic disorder; liver disorder; diabetes;
                                                                                                                                                                                                                             cDNA encoding novel human glycoprotease 28472.
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08-NOV-2000; 2000US-0246772P.
15-NOV-2000; 2000US-0249185P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      myocardial infarction; ischaemic heart disease; Crohn's disease; Graves disease; Kawasaki syndrome; Raynaud's disease; aneurysm; cerebral ischaemia; peripheral neuropathy; Alzheimer's disease; Parkinson's disease; anorexia nervosa; cachexia; glycoprotease;
                                                                                                                                                                                                                                                                                                                                                                                  03-OCT-2002
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DB; ABG71162.
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/product= "Glycoprotease 28472"
/note= "Specifically claimed in claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glycoprotease; gene;
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New adenosine deaminase, glycoprotease and seven transmembrane nucleic acids and polypeptides, designated 38650, 28472, 5495, 81588 and 14354, useful for treating e.g. leukemias, Hodgkin's hypertension. 65507, disease õ

Claim 2; Fig 8A-B; 178pp; English

CC The invention describes isolated 38650, 28472, 5495, 65507, 81588 and CC 14354 nucleic acid molecules (I) and their encoded polypeptides (II). The CC 38650 nucleic acid molecule comprises a sequence encoding adenosine CC deaminase. The 28472 nucleic acid molecule comprises a sequence encoding a human glycoprotease. The 5495, 65507, 81588 and 14354 comprise CC sequences that encode a human seven transmembrane domain (7TM). The CC 38650, 28472, 5495, 65507, 81588 or 14354 nucleic acid and polypeptide CC sequences are useful for diagnosing, preventing or treating a subject CC with or at risk of developing a disorder, e.g. cancer or aberrant CC with or at risk of developing a disorder, e.g. cancer or aberrant CC collular proliferation and/or differential disorders, heart disorders, collular proliferation and/or differential disorders, heart disorders, broan disorders, pain and metabolic disorders, CC cardiovascular disorders, endothelial disorders, heart disorders, collude carcinoma, sarcoma, leukaemia, Hodgkin's disease, autoimune disorders include carcinoma, sarcoma, leukaemia, Hodgkin's disease, autoimune disorders, farction, CC ischaemic heart disease, aneurysm, cerebral ischaemia, peripheral colluderome, Raynaud's disease, aneurysm, cerebral ischaemia, peripheral colluders, Alzheimer's disease, Parkinson's disease, anorexia nervosa, CC cachexia or diabetes. This sequence encodes the novel human glycoprotease

Sequence 1821 B₽; 543 A; 365 ü 394 <u>ن</u> 518 T; 0 1 Other;

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                                                                                      SerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCysHisLeuValLysArg
                                                                                                                                                                                                                                          ASPLYSIleIleMetLysLysGluLysGluGluGlyIleGluLysGlyGlnIleLeuSer
                                                                                                                                                                                                                                                                                                                                                                                             ProPheIleProIleHisHisMetGluAlaHisAlaLeuThrIleArgLeuThrAssnLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AlaLeuSerLeuGlyValGlyLeuSerPheSerLeuGlnLeuValGlyGlnLeuLysLys
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IleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAsp
                                     ThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaVal
                                                                                                                                                                                                                                                                                                        ProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGlyLeuGlnHisValThr
                                                                                                                                                                                                                                                                                                                                                        GlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPheHisPheAspIleLys
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                                                                                                                                         ACACATCGGGCTATTCTGTTTTGTAAGCAGAGAGACTTGTTACCTCAAAATAATGCAGTA
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US-10-649-273-2 (1-414) x ADA52832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases which the gene is involved, or as target molecules for gene therapy.
                                                                                                                                                                                                                                                                                    The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isogai T, Sugiyama T,
Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
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Example 2; SEQ ID NO 7447; 210pp; English.

The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression in the first soft tissue samples and comparing the expression in the first soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.

Sequence 2890 BP; 869 A; 609 ü 611 G; 789 T; 0 U; 12 Other;

Percent Similarity:
Best Local Similarity:
Query Match:
DB: ঠ US-10-649-273-2 (1-414) x ADQ24627 (1-2890) Alignment Pred. No.: 3.2e-193 1944.00 93.24% 93.24% 91.48% Conservative: Mismatches: Indels: Gaps: Length: Matches: 2890 386 0 4 24

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                     IleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAsp
|||||||||
                                                                                      ThrAsnAlaThrGlnCysThrLeuLeuCysProProProArgLeuCysThrAspAsnGly 360
                                                                                                                                                                                                                                                                                                                                               GATAAAATAATGAAAAAGGAAAAAGGGAAGGTATTGAGAAGGGGCAAATCCTGTCT
                                                                                                                                                                                                                                                                                                                                                                 AspLysIleIleMetLysLysGluLysGluGlyIleGluLysGlyGlnIleLeuSer 280
                                                                                                                                                                                                                                                                                                                                                                                                                                           ProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGlyLeuGlnHisValThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPheHisPheAspIleLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProPheIleProIleHisHisMetGluAlaHisAlaLeuThrIleArgLeuThrAsnLys 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AlaLeuSerLeuGlyValGlyLeuSerPheSerLeuGlnLeuValGlyGlnLeuLysLys 140
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                                                                                                                                                                                                       ACACATCGGGCTATTCTGTTTTGTAAGCAGAGACTTGTTACCTCAAAATAATGCAGTA
                                                                                                                                                                                                                                ThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaVal 320
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29-JAN-2002; 2002WO-US001222.

30-JAN-2001; 2001US-00774528

(HYSE-) (GOOD/) HYSEQ INC. GOODRICH R W.

Tang ATY, Liu C, Yang Y, Zhou P, Wehrman Asundi V, 1 T, Wang J, Zhang Wang Ď á Zhao QA, I Drmanac RT,

WPI; 2003-058563/05.

Novel polypeptide useful for treating neurodegenerative diseases, myeloid or lymphoid cell disorders, bone disorders, mechanical and traumatic disorders, coagulation disorders, and inflammatory diseases.

Claim 1; Page; 612pp; English

AIZDELMET'S disease); autoimmune disease (e.g. systemic lupus erythematosus, rheumatoid arthritis, insulin-dependent diabetes mellitus); myeloid or lymphoid cell disorders (e.g. anaemia and thrombocytopaenia); wounds, ulcers, burns, bone disorders (e.g. osteoporosis, osteoarthritis); mechanical and traumatic disorders (e.g. stroke, head trauma); lung or liver fibrosis; reperfusion injury in various tissues; bacterial, viral or fungal infections; allergic conditions such as allergic rhinitis, asthma; coagulation disorders (e.g. haemophilia); cancer and tumours; and inflammatory diseases (e.g. septic shock, Crohn's disease, anaphylaxis). The protein may be used to inhibit the growth, infection or function of infectious agents such as bacteria, fungi, viruses, or to effect bodily characteristics, biorhythms or circadian cycles of rhythms. The protein may also have cycles of rhythms. The protein may also have proliferation/differentiation, stem cell growth lateral sclerosis); neurodegenerative diseases (e.g. Parkinson's disease, Alzheimer's disease); autoimmune disease (e.g. systemic lupus This invention relates to the cDNA sequences encoding an isolated novel human polypeptide. The protein encoded by the nucleic acid of the invention is useful for treating central and peripheral nervous system diseases (e.g. peripheral neuropathy, Huntington's disease, amyotrophic immune stimulating or suppressing, chemotactic/chemokinetic factor, haematopoiesis

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IleGluGlyIleArgTyrGluProLysCysProLeuGlyValAspIleSerLysGluVal 400

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         haemostatic and thrombolytic, receptor/ligand, and antiinflammatory activities. The cDNA sequences of the invention are useful for expressing recombinant protein for analysis. The present sequence represents a novel human cDNA sequence of the invention, this sequence is an expressed sequence tag (EST) and was identified using subtractive hybridisation
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                                                                                                                                                                                                                                                                                                                                                                       ArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProProPro 353
                                                                                                                                          AlaCysHisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeu
                                                                                                                                                                                                       GluLysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMet
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                                                              TTACCTCAAAATAATGCAGTACTGGTTGCATCTGGTGGTGTCGCAAGTAACTTCTATATC
                                                                                                                       GCATGTCATCTTGTGAAAAAGAACACATCGGGCTATTCTGTTTTGTAAGCAGAGAGACTTG
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The present invention describes a non-human transgenic animal (I) CC comprising a disruption in a protease target gene (PG) selected from CC calcium activated neutral protease type 5 (CAPN5) gene, tryptase 4 gene CC and sialoglycoprotease-like gene. Also described is a targeting construct CC (II), comprising a first polymuclectide sequence homologous to at least a CC first portion of PG, a second polymuclectide sequence homologous to at CC least a second portion of PG and a selectable marker. (II) is useful for CC producing a transgenic mouse comprising a disruption in a protease target CC gene, by introducing (II) into a cell introducing the cell into a CC blastocyst, implanting the resulting blastocyst into a pseudopregnant course, where the pseudopregnant mouse gives birth to a chimeric mouse, CC and breeding the chimeric mouse to produce the transgenic mouse. (I) is useful for identifying an agent to the expression or function of a protease target gene, by administering an agent to (I) and CC determining whether the expression or function of the disrupted protease target gene in (I) is modulated. (I) is also useful for testing the cefficacy of proposed genetic and pharmacological therapies for human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAPNS; tryptase 'neurological; neugene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel transgenic animal, comprising a disruption in protease target gene, is useful for identifying agents that ameliorates a phenotype associated with a disruption in a protease target gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Fig 7; 62pp; English.
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06-DEC-2000; 2000US-0251820P.
13-DEC-2000; 2000US-0255971P.
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SerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCysHisLeuValLysArg
                                                                   CCACCTATGCAGAATGCTAAGAATTGCGATTTTTCTTTCACGGGACTTCAACATATTACT
                                                                                 ProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGlyLeuGlnHisValThr
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S

New isolated nucleic acid encoding MP-1 protein, useful for preventing, treating, or ameliorating diseases associated with aberrant metalloproteinse activity, e.g. immune, metabolic, inflammatory and

WPI; 2002-723329/78. P-PSDB; ABG96487.

Chen J,

Feder J,

Nelson

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(BRIM )

BRISTOL-MYERS SQUIBB

05-FEB-2001; 10-APR-2001; 05-FEB-2002;

2001US-0266518P. 2001US-0282814P.

2002WO-US003353

19-SEP-2002 WO200272751-A2

Disclosure; Page 462-463;

473pp;

English

neurological

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Metalloprotease; MP-1; immune disorder; glutamate transport; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding novel human metalloprotease MP1 fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention describes an isolated nucleic acid molecule (I) encoding a metalloprotease (MP-1). (I) is useful for preventing, treating, or ameliorating a medical condition, particularly an immune disorder, an aberrant glutamate transport or motor neuron disorder, such as amyotrophic lateral sclerosis (ALS), its juvenile form or an ALS-like condition. The compositions and methods are also useful for diagnosing, prognosticating, treating, ameliorating and/or treating disorders (e.g., Kleinfelter's syndrome, genital warts, or germinal cell aplasia), metabolic disorders (e.g. premature puberty, Kalman syndrome, or Cushing's syndrome), neurodegenerative diseases (Alzheimer's disease, Huntington's diseases (Alzheimer's disease, Puntington's disease or Tourette syndrome), liver and renal diseases and immune disorders (e.g. AIDS, rheumatoid arthritis or sepsis), pulmonary disease (e.g. premmonia, emphysema or cystic fibrosis) and vascular, inflammatory and neurological disorders (e.g. Alzheimer's disease or Parkinson's disease). This sequence represents a metalloprotease MP1 polynucleotide
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                                                                                                                                                                                                                         ThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeuPhe
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LeuLeuCysProProProArgLeuCysThrAspAsnGlyIleMetIleAlaTrpAsnGly 367
                                                                                 AlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThr
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17-JAN-2002;
17-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnostic and therapeutic polynucleotide; dithp; antiarteriosclerotic; antiinflammatory; cerebroprotective; antiipaemic; antidiabetic; immunosuppressive; neuroprotective; nootropic; neuroleptic; tranquilizer osteopathic; antiarthritic; antirheumatic; cytostatic; hepatotropic; virucide; haemostatic; anti-HIV; antithyroid; thyromimetic; dermatological; antibacterial; fungicide; antiparasitic; anticonvulsant; thrombolytic; anticoagulant; anorectic; vasotropic; antiucer; gene therapy; protein replacement therapy; human; gene; ds.
                                                                             The invention relates to a novel isolated human diagnostic and therapeutic polynucleotide (designated dithp). The novel dithp polynucleotide comprises: any of 188 DNA sequences consisting of 195-779 base pairs fully defined in the specification; a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to the dithp polynucleotide; a polynucleotide complementary to the dithp polynucleotide or its polynucleotide which is at least 90% identical; or an NNA equivalent of any of the polynucleotides mentioned above. The dithp polynucleotides have the following activities:
antiarteriosclerotic, antiinflammatory, cerebroprotective, antilipaemic, antidiabetic, immunosuppressive, neuroprotective, nootropic, neuroleptic tranquilizer, osteopathic, antiarthritic, antirheumatic, cytostatic,
                                                                                                                                                                                                                                                                                                                                                                     Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                New human diagnostic and therapeutic polynucleotides and polypeptides, useful for diagnosing, treating or preventing e.g. leukemia, brain cancer, atherosclerosis, AIDS, thyroiditis, infections, obesity, strok
                                                                                                                                                                                                                                                                                                                                                                                                                               or Alzheimer's.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB;
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CH, Lewis SA, Chen A,
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2002US-0349946P.
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ap PE, Amshey SR, Dam
A, Chen A, Marwaha R,
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m TC, Liu TF, Gerstin
t, Lan RY, Urashka ME;
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"Qy 200	Db 2649 AGAACGTGCTTCGTAAACTAACATACTGCAAAAAAGGTAAAATAAGAGAATATATAT	Фу 200	Db 2709 CATAAAGGCTGAAATAGTTTGCAGATACAGTTATGTATTTTGCCAAATAATGTATGT	Qy 200	Db 2769 GTACACGAATTTATAATTCTTAGCCTTTCTTAATAAATGGTAAGAGGTTCATATCTGTA	Qy 200	Db 2829 TTTTATCTTAGTAAACTGAACACAAAATTCACATATGGTGAGAAAAAATAGAAAGCAGTA	Qy 200	2	200 -		3008	Qy	3067	euThrAsnLysValGluPhe		Conservative: Mismatches: Tridels:	3.39e-94 Length: 1001.50 Matches:	ignment Scores:	Seguen	polynucleotide sequence represents one of the human of the invention.		Huntington's disease, Barkinson's disease, Huntington's disease, Parkinson's disease, anviety schizonhyonial gartypintestinal	hyperlipidaemia, obesity), n	thrombosis, hypon	viral, bacterial, fungal or parasitic infection),	Hashimoto's thyroiditis, multiple sclerosis, osteo	thrombocytopenia), autoimmune/inflammatory discorders (e.g. Addison's discase thyroiditis Crohn's discase Graves'	cancer, preast cancer, cervix cancer, bone cancer, liver cancer) or other cell proliferative disorders (e.g. arterative concernations)	diseases include cancers (e.g. adenocarcinoma, leukaemia,	polypeptides are useful for diagnosing, preventing or		CC hepatotropic, virucide, haemostatic, anti-HIV, antithyroid, thyromimetic cc dermatological, antibacterial, fungicide, antiparasitic, anticonvulsant,
200 Qy 376	2590 Db 1572		2650	1631	2710	1600	2770	296	2830 Db 1810	. Qy 276	200 pb 1870	. 2950 Qy 272	196 Db 1930	3009 Db 1990	176 Qy 241	Db 2050 GGGAAAGC	200	202	Db · 2169	Qy 201	ם bb 2229	, or	disease, Db 2289	emic Oy 200	metabolic Db 2349	sus/, interctions (e.g. Qy 200	Db 2409	Оу 200	sis, Db 2469	brain Qy 200	diseases Db 2529	Фу 200	, Db 2589
1911eLeuHisAspI1eGluGlyI1eArgTyrGluProLysCysProLeuGlyValAspI 396	ATGGCATTATGATTGCATGGAATGGTATTGAAAGACTACGTGCTGGCTTGG 1513	ysThrAspAsnGlyIIeMetIIeAlaTTpAsnGlyIIeGluAfgLeuArgAlaGlyLeuG 3/6		Taleuglui   EleuthrAssAlainrGilnCysinr LeuleuCysbrokrokronagleuc 356				isLeuVallysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuProG 316		lyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCysH 296	GATAAATATTCCTGGATTGTGCCTAAAAATAGCTGCTCATTTCTGCAGGTATTGAGAAGG 1811		TARAKTAATGAAAAAGGAAAAAGGGAAAGGTATATTTCTAATTAGTAAAGTTGAACA 1871	TCATGCTAAAAATTGTGATTTTTCTTTTACTGGACTTCAACACGTTACTGA 1931	oProLeuHisHisAlaLysAsnCysAspPheSerPheThrGlyLeuGlnHisValThrAs       261	GGGGAAAGCCATAGAACATTTGGCCAAACAAGGAAATAGATTTCATTTTGACATCAAACC 1991	GCAAGAAGACITICITIAAIAAAAACAICCAGAGIGCICCACCAIGAGIGGI 2051 allaGluud alaunalaiwaGluGluGaanawaDhaudabaanilaiwaDr 241	AspLysValAlaArgArgLeuSerLeuIleLysHisProGluCysSerThrMetSerGly 221	CCTTTGCATCTTTTCGTTTCACAGTATTTAATTTTATGACTCTAAAAAATATGTTTCTTT 2110	Leu 201	GTATAGCATGTTTTATTCATTCAGGGGTTTTTTGTTTTG	200	ATCATAAGGAACAGGGTTGTCTGCTTACCTGAATATCAGCTATAGTCTATATTTGCCAAA 2230	200	CCAACCAATAGAAGAGCAAACATAGACAGGGGCAGTGATTGGCCTCTTATTGTTCGGGTC 2290	200	ACAAGTTCTTATTATTGACGTTCATCATTAAGCAGTTATTGTCAACTTCAAGCCCCATTTT 2350	200	ATAGGAAACTACAACAACAACGACACGTGCTTCCCCACAGTGAAATAATAGGAAGTATAGG 2410	200	CAGACAGGGTCCCCCCGCACCCCCTTTGTTTTAGAATACTACAGAGGCTACTGCCATAT 2470	200	TTRACATRAGGACATTAAAGATGCAATGCACAGAATTAAATCACACAATTACTTAC

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ABL24633
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                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABE7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                         Sequence 1601 BP; 344 A; 477 C; 441 G; 339 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 25372; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid
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11-JUL-2000; 2000US-00614150.
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                  CGAGTGATTGCCAATGTGCTGGAGTCGCAACAGGAGTTCCACACCCGCTATGGAGGCATT 198
                                                                               GTCCTGGGCATCGAGACCTCCTGCGACGACGACGCGATCGCCATCGTGGACACCACGGGC 138
                                                                                                    ValLeuGlyIleGluThrSerCysAspAspThrAlaAlaAlaValValAspGluThrGly 58
                                              AsnVallencelyGlualarlcHisCerGlaThrGluValHisLeuLysThrGlyGlyIle 78
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                                                                                                                                                                                                                                                                                                                                                                        LeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyValAlaSerAsnPheTyrIle 333
                                                                                               AGCATTGATATCCAGGGCAGCGCGGGATTCGCC
                                                                                                                           GlyValAspIleSerLysGluValGlyGluAla 403
                                                                                                                                                                                                                                             ArgLeuCysThrAspAsnGlyIleMetIleAlaTrpAsnGlyIleGluArgLeuArgAla 373
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          TATATTTGCCAAAGTATAGCATGTTTTATTCATTCAGGGGGTTTTTTTGTTTTGTTAGTAAT
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                                             TATTGTTCGGGTCATCATAAGGAACAGGGTTGTCTGCTTACCTGAATATCAGCTATAGTC
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                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL1640-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                            Sequence 3656
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Search Job ti	DЬ	Ş	DЬ	Ş
Search completed: February 16, 2005, 13:58:31 Job time : 834.4 secs	1465 TGATATCCAGGGCAGCGCGGATTCGCC 1438	394 lAsplieSerLysGluValGlyGluAla 403	1509CTGCAGGATAAAGAGGCCAGCACGCGCTACGACTACGACAGCAT 1466	375 uGlyIleLeuHisAspIleGluGlyIleArgTyrGluProLysCysProLeuGlyVa 394

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Result
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-Q=/cgn2 1/USPTO_spool/US1649273/runat_14022005 114704_16425/app_query.fasta_1.1429
-Q=/cgn2 1/USPTO_spool/US1649273/runat_14022005 114704_16425/app_query.fasta_1.1429
-DB=Issued_Patente_Na -QFMT=fastap -SUPFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bite -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NOREM=ext -HEARSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10649273 @GCN 1 1 292 @runat 14022005 114704 16425 -NCPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

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                                                                                                                                                                                                                 AspLysIleIleMetLysLysGluLysGluGlyIleGluLysGlyGlnIleLeuSer 280
                                                                                                                                                                                                                                                           ProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGlyLeuGlnHisValThr 260
                                                                                                                                                                                                                                                                                                      GlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPheHisPheAspIleLys 240
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                                                                                                              ACACATCGGGCTATTCTGTTTTGTAAGCAGAGAGACTTGTTACCTCAAAATAATGCAGTA
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; LENGTH: 1387
; TYPE: DNA
; ORGANISM: homo s
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Best Local Similarity:
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US-10-649-273-2 (1-414) x US-10-067-443-21 (1-1387)
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GENERAL INFORMATION:
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TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILLING DATE: 2001-02-05
PRIOR FILLING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                               21 GluPheLeuArgSerPheAsnPheHisProGlyThrLeuPheLeuHisLysIleValLeu 40
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                                                                             AlaSerGlyValSerProSerAspLeuSerAlaIleAlaThrThrIleLysProGlyLeu 120
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Sequence 177, Application US/09774528
Patent No. 6743619
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Zhou, Ping
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Asundi, Vinod
APPLICANT: Asing, Jing
APPLICANT: Zhang, Jing
APPLICANT: Zhang, Jing A.
APPLICANT: Zhao, Qing A.
APPLICANT: Yang, Yonghong
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APPLICANT: Wehrman, Tom
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Durui
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6743619el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 802
CURRENT APPLICATION NUMBER: US/09/774,528
CURRENT FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 441
SOFTWARE: pt ft genes Version 2.0
SEQ ID NO 177
LENGTH: 1416
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
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Best Local Similarity:
Query Match:
DB:
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; LOCATION: (205)...
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                                 ThrGlyLeuGlnHisValThraspLysIleIleMetLysLysGluLysGluGluGlyIle
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                                                                                      ArgPheHisPheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPhe
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                                                                            AGATTTCATTTTGACATCAAACCTCCCTTGCATCATGCTAAAAATTGTGATTTTTCTTT
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Matches:
Conservative:
Mismatches:
Indels:
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213 639 193 579 173 153

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GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
ITILE OF INVENTION: POLYNUCLEOTIDE ENCODING A 1
ITILE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                    Pred. No.:
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SEQ ID NO 23
LENGTH: 1526
TYPE: DNA
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1385.00
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TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A P
ITITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.0
SEQ ID NO 20
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Patent No. 6642041
GENERAL INFORMATION:
                                                                                           LENGTH: 14364
TYPE: DNA
ORGANISM: homo
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GENERAL INFORMATION:

APPLICANT:

APPLICANT:

APPLICANT:

PATTERSON, Chandra

APPLICANT:

PATTERSON, CHANDRA

APPLICANT:

PATTERSON:

FILE REFERENCE:

PM-0008-4 US

CURRENT PPLICATION NUMBER: US/09/596,002

CURRENT FILING DATE: 2000-6-16

PRIOR APPLICATION NUMBER: 60/140,121

PRIOR PILING DATE: 1999-06-18
                                                                                                                                                                                                                                                                                 RESULT 6
US-09-596-002-38
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   SOFTWARE:
SEQ ID NO 38
                                                                                                                                                                                                                                            Sequence 38, Application US/09596002 Patent No. 6632636
                                  NUMBER OF SEQ ID NOS:
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                                                                                                                                                   MORAXELLA CATARRHALIS
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; OTHER INFORMATION: Incyte template ID No. 6632636
; PUBLICATION INFORMATION:
US-09-596-002-38
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ThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArg ::: ||||||||::: ||||:::
                                                                                                                                                                SerPheThrGlyLeuGlnHisValThrAspLysIleIleMetLysLysGluLysGluGlu
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                                                                                         GlyIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHis 291
                                                                                                                                                                                                      GGCAACCCACACGCCTATGAGCTGCCAAGACCCCATGCAGCAT----AAAGGGCTGGATTTT
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; ORGANISM: M.catarrhalis
US-09-540-236-806
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Best Local Similarity:
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APPLICANT: GATY L. Breton et al.
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAFITTLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT PILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 806
LENGTH: 1053
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316 GCGTATGGGCTGGGCGTGCCAGCGGTTGGGGTGCATCATATGGAGGGACATCTGTTAGCA 375
                                   135
                                                                                              115 ThrIleLysProGlyLeuAlaLeuSerLeuGlyValGlyLeuSerPheSerLeuGlnLeu 134
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                                ValGlyGlnLeuLysLysProPheIleProIleHisHisMetGluAlaHisAlaLeuThr 154
                                                                                                                                                                 ValGlnGluAlaLeuSerAlaSerGlyValSerProSerAspLeuSerAlaIleAlaThr 114
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                                                                     ACCAAAGGCCCCGGGCTGATTGGGGGCATTGATGACAGGGGCATTATTTGGGCGGACGCTG
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             SEQ ID NO 801
LENGTH: 1206
TYPE: DNA
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APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                    sequence 801, Application US/09252991A
Patent No. 6551795
                                                                 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142
                                                                                                                    CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18
ORGANISM: Pseudomonas aeruginosa
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Percent Similarity:
Best Local Similarity:
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 884
LENGTH: 1059
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity:
Query Match:
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US-09-252-991A-884/c
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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TYPE: DNA
ORGANISM: Proteus mirabilis
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ThrAspAsnGlyIleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeu---
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                                                                     LeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProProArgLeuCys 356
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                                           ATGGCGATGATAATGGAACAACTCGGAGGGGAAGTGTTTTATGCTCGCCCTGAGTTATGT
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Sequence 6612, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Seco
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Best Local Similarity:
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CTCGTCCTAGGACTGGAAACCTCGTGTGATGAGACTGCCGCCGCCGTCGTGGAGGACGGC
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                                                      ProGlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGluCys
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                                                                                                                Percent Similarity:
Best Local Similarity:
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                                                                                                                                                               Pred. No.:
                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                         US-09-902-540-503
                                                                                                                                                                                                                                                  SEQ ID NO 503
LENGTH: 2582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 503, Application US/09902540 Patent No. 6833447
                                                                                                                                                                                                                                                                                                                  APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
CURRENT FILING DATE: 2001-07-10
                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
                                                                                                                                                                                                                   LENGTH: 2582
TYPE: DNA
ORGANISM: Myxococcus xanthus
1525 CTCGTCCTAGGACTGGAAACCTCGTGTGAGACTGCCGCCGCCGCCGTCGTGGAGGACGGC 1466
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Matches:
Conservative:
Mismatches:
Indels:
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US-08-087-797-1
Sequence 1, Application US/08087797 Patent No. 5543312 GENERAL INFORMATION:
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DB:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1315 base pairs
TYPB: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTINE PATENT RELEASE #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,797
FILING DATE: 14-JUL-1993
CLASSIFICATION: 435
ATTORNEY/AGENT IMPORMATION:
NAME: Layton, Jr., Samuel G.
REGISTRATION NUMBER: 3374-80
TELECOMMUNICATION INFORMATION:
TELEPHONE: 704 377 1561
TELEPHONE: 704 377 1561
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HYPOTHETICAL: N
ANTI-SENSE: NO
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NAME/KEY:
LOCATION:
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APPLICANT: Lo, Reggie Y.C.
APPLICANT: Abdullah, Khalid M.
TITLE OF INVENTION: Pasteurella Haemolytica
TITLE OF INVENTION: Glycoprotease
TITLE OF INVENTION: Gene and the Purified Enzyme
NUMBER OF SEQUENCES: 3
ANDERSES: BOLLER BALL Giber Ball
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Charlotte
STATE: No. 5543312th Carolina
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  296 CCGTAAAACGTTGCCACTAATTCAAGAAGCCTTAAAAGAGGCCAATCTGCAACCCTCGGA 355
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                           gGluAsnIleGlnArgIleValGlnGluAlaLeuSerAlaSerGlyValSerProSerAs 108
                                                                                 AATTGATATGCACGCGATTACGGTGGCUTAGTCCCTGAACTGGCTTCTCGAGACCATAT 295
                                                                                                      nThrGluValHisLeuLysThrGlyGlyIleValProProAlaAlaGlnGlnLeuHisAr
                                                                                                                                                                                              pThrAlaAlaAlaValValAspGluThrGlyAsnValLeuGlyGluAlaIleHisSerGl
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48.63%
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22.54%
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RESULT 14
US-09-557-884-1/c
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3-09-557-884-1/c
Sequence 1, Application US/09557884
Patent No. 6506581
GENERAL INFORMATION:
Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae of the Haemophilus in
  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1082
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Best Local Similarity:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: <Unknown>
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REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
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APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
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GlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGluCysSer
                                                                                        GTGCGTGTCGATGGTGTAGGAAAATATGAAGTGATAGGAGAATCTATTGATGATGATGCTGCT
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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KEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOPTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                           APPLICATION NUMBER: 08/487,429
PILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
PILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESCONDENCE ADDRESSE: 1
ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
CITY: Rockville,
                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/643,990A
PILING DATE: 23-Aug-2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: MD
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                              NAME: Kenley K. Hoover REGISTRATION NUMBER: 4
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REFERENCE/DOCKET NUMBER: PB186P1C1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Owen White
Hamilton O. Smith
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TELEPAX: 310-309-6439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            552788 GTGCGTGTCGATGGTAGGAAAATATGAAGTGATAGGAGAATCTATTGATGATGATGCTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198
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                                                                                                                                                                                                                            AspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGlyLeuGln 257
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ACATTTCCACGTCCAATGACAGATCGTGCAGGCCTTGATTTTAGTTTTTTCTGGTTTTAAAA 552570
                                                                                                                                                                                                                                                                                                                                                                                                    ThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPheHisPhe
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                                       GlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCys
                                                                                                               <u>ACATTTOCCCCAAATACAGTTAATCAAGCAATTAAAAAACGAGGGCGAACTGATAGAGCAA</u>
                                                                                                                                                                                                                                                                                                                                              ------GITGGCGCACTTTCTCGTTTAGCGGAAAAAGGTACGCCAAATCGTTTC 552630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGluCysSer 217
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                                                                                                                                                   HisValThrAspLysIleIleMetLysLysGluLysGluGluGly-----IleGluLys 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGCTTGTTGGCGCATTGCTTGTCGGTGCTACGATTGCACGTTCTTTAGCCTATGCTTGG
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STRANDEDNESS: double
TOPOLOGY: linear
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ACTAAAGCAGATATTGCTTATGCTTTCCAAGATGCGGTGGTGGAT 552465
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316 GlnāsnāsnālaValLeuValālaSerGlyGlyValālaSerāsnÞheTyrIleArgārg 335
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552428 ACAGGCTATAAACGTTTAGTGATTGCGGGAGGGGGTGAGCGCAAATAAAAAACTCCGAGAA 552369
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Search completed: February 16, 2005, 21:50:50 Job time : 2493.15 secs

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-Q-/G912 1/USPTO spool/USI0649273/runat 14022005 114706 16497/app query.fasta_1.1429
-Q-/G912 1/USPTO spool/USI0649273/runat 14022005 114706 16497/app query.fasta_1.1429
-DB=Published Applications NA -QFMT=fastap -SUPFIX=rnpb-MINMATCH=0.1
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10649273 @CGN 1 1 1053 @TUNat 14022005 114706_16497
-NCYDU=6 -TCPU=3 -NO MAAP -LARGSQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPEOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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Pred. No. is the number of results predicted by chance to have a score greater than or emual to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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## ALIGNMENTS

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Sequence 1, Application US/10067443

Publication No. US20030082782A1

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT APPLICATION NUMBER: US/60/266,518
FRIOR PILING DATE: 2001-02-05
PRIOR PILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR PILING DATE: 2001-04-10
NUMBER: OF SEC ID NOS: 71
SOPTWARE: PatentIn version 3.0
SEO ID NO 1
LENGTH: 2197
TYPB: DNA
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Alignment Scores:
Pred. No.:
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Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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; FRATURE:
; NAME/KEY: CDS
; LOCATION: (231)..(1472)
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           ABPLYSIleIleMetLySLYSGluLySGluGlyIleGluLySGlyGlnIleLeuSer
                                  SerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCysHisLeuValLysArg
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GlyGluAlaSerIleLysValProGlnLeuLysMetGluIle 414
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CORGANIEM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (231)..(1472)
US-10-651-722-1
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Publication No. US20040048302A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
FILE OF INVENTION: POLYNUCLEOTIDE ENCODING A N
FILE REFERENCE: D0073 DIV
CURRENT APPLICATION NUMBER: US/10/651,722
CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/67,443
PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PAtentin version 3.2
SEQ ID NO 1
LENGTH: 2197
TYDE: DNA
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ValGluPheProPheLeuValLeuLeuIleSerGlyGlyHisCysLeuLeuAlaLeuVal
                                                       ProPheIleProIleHisHisMetGluAlaHisAlaLeuThrIleArgLeuThrAsnLys
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Sequence 21, Application US/10067443

Publication No. US20030082782A1

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED I
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: DO073 NP
CURRENT APPLICATION NUMBER: US/10/067,443

CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-04-10

NUMBER OF SEQ ID NOS: 71
SOPTWARE: Patentin version 3.0

SEQ ID NO 21
LENGTH: 1387
TYPE: DNA
ORGANISM: homo sapiens

US-10-067-443-21
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                                          CAGATAAATATTCCTGGATTGTGCCTAAAAATAGCTGCTCATTTCTGCAGGTATGAGAAG
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Sequence 21, Application US/10649273

Publication No. US20040043407A1

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
ITILE OF INVENTION: POLYNUCLECTIDE ENCODING A N
PILE REFERENCE: D0073 CNT
CURRENT APPLICATION UNMBER: US/10/649,273

CURRENT FILING DATE: 2003-08-27

PRIOR APPLICATION NUMBER: US 60/266,518

PRIOR FILING DATE: 2001-02-05

PRIOR APPLICATION NUMBER: US 10/067,443

PRIOR FILING DATE: 2002-02-05

PRIOR APPLICATION NUMBER: US 60/282,814

PRIOR FILING DATE: 2001-04-10

NUMBER OF SEQ ID NOS: 71

SOFTWARE: PATENTIN PRIOR STATE: 1387

TYPE: DNA
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Best Local Similarity:
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CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR PILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-649-273-2 (1-414) x US-10-651-722-21 (1-1387)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 21
LENGTH: 1387
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Publication No. US20040048302A1
GENERAL INFORMATION:
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TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
FILE REFERENCE: D0073 DIV
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                                              ValGluPheProPheLeuValLeuLeuIleSerGlyGlyHisCysLeuLeuAlaLeuVal 180
                                                                                            ProPheIleProIleHisHisMetGluAlaHisAlaLeuThrIleArgLeuThrAsnLys
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Sequence 6, Application US/10012140

Publication No. US20030099017A1

GENERAL INFORMATION:
APPLICANT: Leiby, Kevin R.
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Glucksmann, Maria A.
ITILE OF INVENTION: 38650, 28472, 5495, 65507, 81588, AND
ITILE OF INVENTION: 14354 METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND CURRENT APPLICATION NUMBER: US/10/012,140

CURRENT APPLICATION NUMBER: US/10/012,140

CURRENT FILING DATE: 2001-11-08

PRIOR APPLICATION NUMBER: 60/246,768

PRIOR APPLICATION NUMBER: 60/246,772

PRIOR APPLICATION NUMBER: 60/246,772

PRIOR PILING DATE: 2000-11-08

PRIOR FILING DATE: 2000-11-08

PRIOR FILING DATE: 2000-11-18

PRIOR FILING DATE: 2000-11-18

PRIOR FILING DATE: 2000-11-18

PRIOR FILING DATE: 2000-11-15

NUMBER OF SEQ ID NOS: 49

SOFTWARE: FastSEQ for Windows Version 4.0
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SerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCysHisLeuValLysArg 300
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                                                AspLysIleIleMetLysLysGluLysGluGluGlyIleGluLysGlyGlnIleLeuSer 280
                                                                                  ProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGlyLeuGlnHisValThr 260
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Sequence 4, Application US/10012140

Publication No. US20030009017A1

GENERAL INFORMATION:
APPLICANT: Leiby, Kevin R.
APPLICANT: Leiby, Kevin R.
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Gelucksmann, Maria A.
TITLE OF INVERTION: 14354 METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND USES
TITLE OF INVERTION: THEREOF
FILE REPERENCE: 38155204900
CURRENT APPLICATION NUMBER: US/10/012,140
CURRENT APPLICATION NUMBER: 60/246,768
PRIOR APPLICATION NUMBER: 60/246,768
PRIOR APPLICATION NUMBER: 60/246,772
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/246,772
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 49
SOPTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                       LENGTH: 1820
; TYPE: DNA
; ORGANISM: Homo sapiens
; PEATURE:
; NAME/KEY: CDS
; LOCATION: (146)...(1390)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1820)
; OTHER INFORMATION: n = A,T,C or
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US-10-649-273-2 (1-414) x US-10-012-140-4 (1-1820)
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APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA; MOTOYUKI
APPLICANT: UNACHARI, KENJI
APPLICANT: UNACHARI, KENJI
APPLICANT: WASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR FILING DATE: 2002-03-12
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-14
UNDBER OF SEQ ID NOS: 3381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOPTWARE: Patentin Ver. 2.1
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LENGTH: 2208
TYPE: DNA
ORGANISM: Homo sapiens
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SATO, HIROYUKI
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IRIE, RYOTARO
TAMECHIKA, ICHI
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YAMAMOTO, JUN-ICHI
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GENERAL INFORMATION:

APPLICANT: Aziz, Natasha

APPLICANT: Ginsburg, Wendy M.

APPLICANT: Zlotnik, Albert

TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions & TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma Modulators

FILE REFERENCE: 05882.0193.NPU901

CURRENT APPLICATION NUMBER: US/10/723,860

CURRENT PILING DATE: 2003-11-26

PRIOR APPLICATION NUMBER: 60/429,739

PRIOR FILING DATE: 2002-11-26

NUMBER OF SEQ ID NOS: 8393

SOFTWARE: PAtentIn version 3.2

SEQ ID NO 7447

LENGTH: 2890

TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:

NAME/KEY: misc_feature
LOCATION: (646)..(657)

OTHER INFORMATION: n is a, c, g, or t
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Query Match:
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GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: Geodrich, Ryle

APPLICANT: Liu, Chenghua

APPLICANT: Liu, Chenghua

APPLICANT: Ren, Feiyan

APPLICANT: Wang, Dunrui

APPLICANT: Drmanac, Radoje T.

TITLE OF INVENTION: No. US20030219745A1el Nucleic Aci

TITLE OF INVENTION: Polypeptides

FILE REFERENCE: 802CON

CURRENT APPLICATION NUMBER: US/10/120,988

CURRENT FILING DATE: 2002-04-11

PRIOR APPLICATION NUMBER: 09/774,528

PRIOR FILING DATE: 2001-01-30

NUMBER OF SEQ ID NOS: 441

SOFTMARE: pt_FL_genes Version 2.0

SEQ ID NO 177

LENGTH: 1416

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: CDS

LOCATION: (205)..(1305)
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; LENGTH: 1526
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Publication No. US20030082782A1

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/262,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.0
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                   ThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeuPhe 307
                                                                          GluLysGluGluGlyIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAla
                                                                                                                                 AsnCysAspPheSerPheThrGlyLeuGlnHisValThrAspLysIleIleMetLysLys
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                                                                                                                  AATTGTGATTTTTCTTTTACTGGACTTCAACACGTTACTGATAAAATAATAATGAAAAAG
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LENGTH: 1526
TYPE: DNA
ORGANISM: homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bristol-Myers Squibb Company TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING FILE REFERENCE: D0073 CNT CURRENT APPLICATION NUMBER: US/10/649,273 CURRENT FILING DATE: 2003-08-27
                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.2
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APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-
FILE REFERENCE: DO073 DIV
CURRENT APPLICATION NUMBER: US/10/651,722
CURRENT APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2002-02-05
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.2
SEQ ID NO 23
LENGTH: 1526
TYPE: DNA
ORGANISM: homo sapiens
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             Length:
Matches:
Conservative:
Mismatches:
Indels:
 Gaps:
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Sequence 20, Application US/10067443
Publication No. US20030082782A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A 1
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/282,814
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CCATTT CTTGTACTAGTTTGGTAGCTTTATGGGACAGCTGTATAGCTTCTATGGCACATA	Qy 204 204 Pp
12362 CITTATIGCUTTATGCCCTGACAGTATGAAATTATGCAGGATAGGAAAGACTAACAG 12921	Db 11282 ATGTGAAAGAACGTGCTTCGTAAACTTAACATACTGCAAAAAAGGTAAAATAAGAGAAATAT 11341
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CACTTTGCAATATGTTACTTTTTTCCCAAGACCTTGACCTTGTGTTTTAGGATGAACAGAT	Db 11222 ATCTGTACATAAAGGCTGAAATAGTTTGCAGATACAGTTATGTATTTTGCCAAATAATGT 11281
321	Оу 204 204
CTTGTTACCTCAAAATAATGCAGTACTGGTAAGTTTTATCTCATTTTATAGTAATAGTTA	Db 11162 AAGAGTAGTACACAATTTTATAATTCTTAGCCTTTCTTAATAAAATGGTAAGAGGTTCAT 11221
312 pLeuLeuProGlnAsnAsnAlaValLeu	204
12182 AATGGCATGTCATCTTGTGAAAAGAACACATCGGGCTATTCTGTTTTGTAAGCAGAGAGA 12241	Db 11102 TATTTCTGAATTTTATCTTAGTAAACTGAAAAAAATTCACATATGGTGAGAAAAAATAGA 11161
292 rMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAs 312	20A
	AGCA
	Qy 194 AspIleAlaProGlyAspMetLeuAspLysVal 204
	Qy       174 HisCysLeuLeuAlaLeuValGlnGlyValSerAspPheLeuLeuGlyLysSerLeu       193
11942 GACATCAAACCTCCCTTGCATCATGCTAAAAATTGTGATTTTTCTTTTACTGGACTTCAA 12001 258 HisValThrAspLysIleIleMetLysLysGluLysGluGlu 271	10863 ACTATTAGGTTGACCAATAAAGTAGAATTTCCTTTTTAGTTCTTTTGATTTCTGGAGGT
238 AspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGlyLeuGln 257	154 ThrIleArgLeuThrAsnLysValGluPheProPheLeuValLeuLeuIleSerGlyGly
ACCATGAGTGGTGGGAAAGCCATAGAACATTTGGCCAAACAAGGAAATAGATTTCATTTT	Qy       134 LeuValGlyGlnLeuLysLysProPheIleProIleHisHisMetGlualaHisAlaLeu 153
11822 AATATGTTTCTTTGATAGGTGGCAAGAAGACTTTCTTTAATAAAACATCCAGAGTGCTCC 11881 218 ThrMetSerGlvGlvLvsalaTleGlnHisLenalafvsGlnGlvAsnargDheHisDhe 237	Db 10743 ACTACCATAAAACCAGGACTTGCTTTAAGCCTGGGAGTGGGCTTATCATTTAGCTTACAG 10802
205AlaArgArgLeuSerLeuIleLysHisProGluCysSer 217	114 ThrThrIleLysProGlyLeuAlaLeuSerLeuGlyValGlyLeuSerPheSerLeuGln 133
11762 TTTCAATTTATTTCCTTTGCATCTTTTCGTTTCACAGTATTTAATTTTATGACTCTAAAA 11821	106
204 204	40 TipValGinglalarangarangarangarangarangarangarang
11702 TATATTTGCCAAAGTATAGCATGTTTTATTCATTCAGGGGTTTTTTGTTTTGTTAGTAAT 11761	74 LysThnGlyGlyIIeValProProAlaAlaGlnGlnLeuHisArgGluAsnIIeGlnArg 93 
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11642 TATTGTTCGGGTCATCATAAGGAACAGGGTTGTCTGCTTACCTGAATATCAGCTATAGTC 11701	Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Capana Ca
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204 204	. 7.32e-132 Length:
11522 TAGGAAGTATAGGACAAGTTCTTATTATTGACGTTCATCATTAAGCAGTTATTGTCAACT 11581	Alignment Scores.
204 204	y ORGANISM: homo sapiens Qy
11462 GCCATATATAGGAAAACAAACAAACAAACAAACAAACACTGCTTCCCACAGTGAAATAA 11521	; SEQ 1D NO 20 ; LENGTH: 14364 ; TYPE: DNA
204 204	; SOFTWARE: PatentIn version 3.0  Qy
11402 TACACCACAGACAGGGTCCCCCCCCCCCCCTTTGTTTTAGAATACTACAGAGGCTACT 11461	PRIOR FILING DATE: 2001-04-10 Db

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ProProArgLeuCysThrAspAsnGl 360	uThrAsnAlaThrGlnCysThrLeuLeuCysPro	340	Ś
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D97677
E977677
E977677
AB3274
F87257
T1825
G70369
H83572
C91125
B85967
QQECR6
AG0892
AI0079
A381089
A610892
AI0079
B97011
C8104074
B97011986
C81986
C91988
B4707888
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probable O-sialogl
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probable glycoprot
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probable o-sialogl
O-sialoglycoprotei
probable o-sialogl
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                                                                                                                                                                                                                                                                                                                                C;Genetics:
A;Gene: At2g45270
A;Gene: Ac2g45270
                                                                                                                                                                                                                                                                                                                                                          probable O-sialoglycoprotein endopeptidase [imported] - Arabidopsis thaliana C.Species: Arabidopsis thaliana (mouse-ear cress) C.Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Jun-2003 C.Accession: B84888 R.Lin, X., Kaul, S.; Rounsley, S.D.; Shea, T.P., Benito, M.I.; Town, C.D.; Fujii, C.Y.; N., Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999 A.;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A.;Accession: E84888 A.;Accession: E84888 A.;Accession: E84888 A.;Accession: E84888 A.;Cross-references: GB:AE002093; NID:g2583127; PIDN:AAB82636.1; GSPDB:GN00139 C.Centrics: references: GB:AE002093; NID:g2583127; PIDN:AAB82636.1; GSPDB:GN00139
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C;Superfamily: O-sialoglycoprotein endopeptidase
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E84888
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Best Local Similarity
Matches 145; Conserv
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437.5
430.5
409.5
409.5
406.5
406.5
400.5
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3391.5
3391.5
331.5
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                                                                                                                                                                                                                                                                              ch 29.8%; Score 634; DB 2; al Similarity 37.9%; Pred. No. 2e-43; 145; Conservative 61; Mismatches 129
                                                                                                                                                     LEILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDIEGIRYB------
                                                                       --IRNRADIAASFORVAVLHLBEKCERAIDWALE---LEPSIKHMVISGGVASNKYVRLR 363
                                                                                    QILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLFQNNAVLVASGGVASNFYIRRA
                                                                                                                           STMSGGKAIEHLAKQGNRFHFDIKPFLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKG
                                                                                                                                                                                             ALDKANLTEKDLSAVAVTIGPGLSLCLRVGVRKARRVAGNFSLPIVGVHIMEAHALVARL
                                                                                                                                                                                                         ALSASGVSPSDLSAIATTIKPGLALSLGVGLSFSLQLVGQLKKPFIPIHHMEAHALTIRL
                                                                                                                                                                                                                                       VIGIETSCDDTAAAVVSPFNHLSSSC---RAELLVQYGGVAPKQAEEAHSRVIDKVVQD
                                                                                                                --RSGGPAVEELALEGDAKSVKFNVPMKYHKDCNPSYAGLKTQVRLAIEAKE-----
                                 LINIVENKULKLVCPPPSLCTDNGVMVAWTGLEHPRVG---
  ----PKCPLGVDISKBVGBA
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TAB2807
D82807
G89996
H71545
H72106
B86515
T35581
G86561
G86561
E81278
E81278
F90526
A64205
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             403
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probable o-sialogl
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hypothetical prote
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Gaps

413

308

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A;Residues: 1-387 <AND>
A;Cross-references: UNIFA
A;Cross-references: structure: st
C;Genetics:
A;Gene: gcp; RP037
C;Superfamily: O-sialogly
                                                                                                                                                       C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AB2902
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, P.; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Goi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable o-sialoglycoprotein endopeptidase (gcp) RP037 - Rickettsia prowazekii C,Species: Rickettsia prowazekii C,Species: Rickettsia prowazekii C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004 C;Accession: E71711 R,Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature 396, 133-140, 1998 Nature 396, 133-140, 1998 Nature 396, 133-140, 1998 Nature 396, 133-140, 1998 Nature 396, 133-170, Nature 396, 133-170, Nature 396, 133-170, Nature 396, 133-170, Nature 396, 133-170, Nature 396, 133-170, Nature 396, 133-170, Nature 396, Nat
A;Title: The Genome of the Natural Genetic A;Reference number: AB2577; MUID:21608550; A;Accession: AB2902
A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                             O-sialoglycoprotein endopeptidase gcp [imported] - Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens
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Best Local S
Matches 133
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Experimental source: strain Madrid B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NWKPLECITRPKYRIHIQNSYRSNLLNDTIVIAGGVAANKYLQEILSDCTRPYGYRLIAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -SFPGGPEIEKRAKLGNPHKYKFPKPIINSGNCNMSFSGLKTAVRTLIMNLKEVNDSV--
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                                                                                                                                                                                P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
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                                                                                                Engineer Agrobacterium PMID:11743193
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RESULT 4
D97677
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A;Cross-references: GB:AE008688; PIDN:AAL43632.1; PID:g17741154; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
C;Genetics:
C;Genetics:
A;Gene: gcp
A;Map position: circular chromosome
C;Superfamily: O-sialoglycoprotein endopeptidase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                       329
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                                                                                                               KCPLGVDISKE 399
                                                                                                                                                  ANQEIRQTLQALCOTHGFRFVAPPHRLCTDNAAMIAWAGLERMAEG----RQADALEVAP
                                                                                                                                                                                   SNFYIRRALBILINATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDIEGIRYEP
                                                                                                                                                                                                                          ------IADICASFOKAVSRTLKDRIGRGLARFKVE--FPHINGEPALVVAGGVA
                                                                                                                                                                                                                                                                 EGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNA--VLVASGGVA
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                                                                                                                                                                                                                                                                                                    25.8%;
36.9%;
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Pred. No. 1.3e-36;
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A; Reference number: A97359; MUID:21608551; PMID:117
A; Accession: D97677
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-366 < KUR>
A; Cross-references: GB:AE007869; PIDN:AAK88373.1; P
C; Genetics:
A; Gene: AGR C 4806
A; Map position: circular chromosome
C; Superfamily: O-sialoglycoprotein endopeptidase R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quro. A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, Science 294, 2323-2328, 2001 probable o-sialoglycoprotein endopeptidase (glycoproteinase) [imported] - A C;Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 18-Nov-2002 C;Accession: D97677 A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A;Reference number: A97359; MUID:21608551; PMID:11743194 Matches Query Match Best Local : Local Similarity 89 95 39 VLGIETSCDDTAAAVV----DETGNVLGEAIHSQTEVHLKTGGIVPPAAQQLHRENIQRI : | | | | | | | | | | | | : : : : | | | | | | : | | | : : : : : | | | | | | : | | | | : | | | : : : : : : | | | | | | : | | | | : | | | : : : : : : | | | | | | : | | | : | | : : : : : : | | | | | : | | | : | | : : : : : : | | | | | : | | : | | : : : : : : | | | | | : | | : | | : : : : : : | | | | | : | | : | | : : : : : | | | | : | | : : : : : : | | | | | : | | : | : : : : : : | | | | : | : : : : : : | | | | : : : : : : | | | | : | | : : : : : : : | | | | : | : : : : : : | | | | : | : : : : : : | | | | : | : : : : : : : | | | | : | : : : : : : : | | | | : | : : : : : : | | | | : | : : : : : : | | | | : | : : : : : : | | | | : | : : : : : : | | | | : | : : : : : : | | | | : | : : : : : : | | | | : | : : : : : : | | | | : | : : : : : : | | | | : | : : : : : : | | | | : | : : : : : : | | | | : | : : : : : : | | | | : | : : : : : : | | | | : | : : : : : : | | | | : | : : : : : | | | | : | : : : : : : | | | | : | : : : : : : : | | | | : : : : : : : : | | | | : : : : : : : | | | | : | : : : : : : : | | | | : | : : : : : : : | | | | : | : : : : : : : | | | | : | : : : : : : : | | | | : | : | | : | : : : : : : | | | | : | | : | : : : : : : : | | | | : | | : | : | | : | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | | : | : | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : : : : : : : | : | : | : | : | : | : | : | : | : | : | : | : 137; VQEALSASGVSPSDLSAIATTIKPGLALSIGVGLSFSLQLVGQLKKPFIPIHHMEAHALT 154 ILGIETSCDETAASIVVRHADGRGEIVSDVVLSQLEEHSAYGGVVPEIAARAHVEALDTL VERALDQAGVKLADVDATAATSGPGLIGGLLVGLMTGKATAKAAGKPLYATNHLEGHALT Conservative GB:AE007869; PIDN:AAK88373.1; PID:g15157858; GSPDB:GN00169 25.8%; Score 548; DB 2; 36.9%; Pred. No. 1.3e-36; 58; Mismatches 142; Length 366; Indels 34; Qurollo, B.; Gold ppas, C.; Markelz, Gaps Agrobacterium 127 67 94 Goldman, ckelz, B.;

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O-sialoglycoprotein endopeptidase (EC 3.4.24.57) [imported] - Rickettsia conorii (Strain (Species: Rickettsia conorii (C;Species: Rickettsia conorii (C;Date: 30-Sep_2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001 (C;Accession: B97707 R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Rd Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Recession: B97707
A;Status: preliminary A;Status: preliminary A;Status: preliminary A;Cross-references: GB:AE006914; PIDN:AAL02599.1; PID:g15619097; GSPDB:GN00173
A;Cross-references: GB:AE006914; PIDN:AAL02599.1; PID:g15619097; GSPDB:GN00173
C;Genetics: A;Gene: GC;Copportein endopeptidase
C;Keywords: hydrolase; metalloproteinase
RESULT
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                                                                                                            LEILTNATQCTLLCPPPRLCTDNGIMIAWNGIER 370
                                                                                                                                                                                                                                                                                                 MSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMK-KEKEEGIEKGQ
                                                                                                                                                                                                                                                                                                                                                                                                                               LKESNTKLTDISTIAATSGPGLIGGVIVGSMPARSLSSALKKPPIAINHLEGHALTARLT
                                                                                   LSSCAKTYGYRLIYPPIHLCTDNAAMIAYAGLER 320
                                                                                                                                                                       ----INDIAASFQFTIGEILSSKVQDAIRAYEQITNNFDKKN--IVIAGGVAANKYLQKI 286
                                                                                                                                                                                                             ILSSAADIAATVOHTMACHLVKRTHRAILFCKQ-RDLLPQNNAVLVASGGVASNFYIRRA 336
                                                                                                                                                                                                                                                           FPGGPEIEKRAKLGDPHKYKPPKPIINSGNCNMSFSGLKTAVRTLIMTLKBINDTV----
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O-sialoglycoprotein endopeptidase (EC.3.4.24.57) [imported] - Brucella melitensis (strair C;Species: Brucella melitensis
C;Species: Brucella melitensis
C;Jate: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
C;Accession: AB3274
R,DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, N.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessc Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A,Title: The genome sequence of the 43-448, 2002
A,Title: The genome sequence of the 43-448, 2002
A,Reference number: AD3252; PMID:11756688
                                                                                                                                                                                             R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.I. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolong n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: F87257
                                                                                                                A; Molecule type: DNA
A; Residues: 1-367 < STO>
                                                                                                                                                                                                                                                                                                                                                                                                       peptidase M22 family protein [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001 C;Accession: F87257
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C; Superfamily: O-sialoglycoprotein endopeptidase
C; Keywords: hydrolase; metalloproteinase
C; Superfamily:
                                A;Gene: CC0071
                                                           C;Genetics:
                                                                                   A; Cross-references: GB: AE005673; NID: g13421168;
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A;Experimental source: strain 16M
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A; Residues: 1-359 < KUR >
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Best Local Similarity
Matches 132; Conserv
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  O-sialoglycoprotein endopeptidase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.4%; Score 539.5; DB 2; 38.6%; Pred. No. 6.3e-36; tive 52; Mismatches 127;
                                                                                      PIDN:AAK22058.1; GSPDB:GN00148
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Best Local Similarity

25.2%;

Score 535.5; DB 2; Pred. No. 1.4e-35;

Length 367;

Query Match

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A;Molecule type: DNA
A;Residues: 1-421 <WIL>
A;Cross-references: EMBL:Z81030; PIDN:CAB02716.1; GSPDB:GN00023; CESP:C01G10.10
A;Experimental source: clone C01G10
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein C01G10.10 - Caenorhabditis elegans C;Specites: Caenorhabditis elegans C;Specites: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000 C;Accession: T18825 R;Matthews, L.
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A;Introns: 31/2; 72/3; 122/2; 177/1; 272/3; 315/1; 353/2
C;Superfamily: O-sialoglycoprotein endopeptidase
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A;Reference number: Z19027
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   RALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIBRLRAGLGILHDIEGIRYEP-----
                                                                                                                                                                                                                      GIHVGAAVEILASRASADGHLRYPIFLPNVPKANMNFDQIKGSYLNLLERLRKNSETSID
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                                                                                                                                                KGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNFYIR 334
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RESULT
G70369
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C;Species: Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: G70369
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C;Superfamily: O-sialoglycoprotein endopeptidase
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A;Accession: G70369
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A; Residues: 1-335 < AQF >
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---EDIAYSFQETVVEILLEKS----LWAMKKTGIKR----LVVVGGVSANSRLR----EV
                                                                                                                              SSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRALEI 339
                                                                                                                                                                                                                                                                                                               KVEFPFLVILISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTM 219
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                                                                                                                                                                                   -GGPIIDRLAKEGKKL-YPLPKPLMEEGNLNFSFSGLK---TAILNLLKKEKNVRK----
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LMLVNRSEAIWWRPNDIPDT 367
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SULT 10

O-sialoglycoprotein endopeptidase PA0580 [imported] - Pseudomonas aeruginosa (strain PAO] C;Species: Pseudomonas aeruginosa (c;Species: Pseudomonas aeruginosa (c;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000 C;Accession: H83572 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Briadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Polger, K.R.; Kas, A.; Larbig, K.; Lim, J.Cry, S.; Olson, M.V.; Nature 406, 959-964, 2000 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog R;Reference number: A82950; MUID:20437337; PMID:10984043 A;Status; preliminary

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C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: C91122
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gual a, Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: C91122
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-337 <HAY>
A;Residues: 1-337 <HAY>
A;Resperimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: EC53947
C;Superfamily: O-sialoglycoprotein endopeptidase
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A;Residues: 1-341 <STO>
A;Cross references: GB:AE004494; GB:AE004091; NID:g9946446; PIDN:AAG03969.1; GSPDB:GN001
A;Experimental source: strain PAO1
C;Genetics: PA0580
A;Gene: gcp; PA0580
C;Superfamily: O-sialoglycoprotein endopeptidase
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Best Local S
Matches 128
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                              THKVEFPFLYLLISGCHCLLALVQGYSDFLLIGKSLDIAFGUMLDKVARRLSLIKHPECS 217
                                                                                                                                                                                                      LSASGVSPSDLSAIATTIKPGLALSLGVGLSPSLQLVGQLKKPPIPIHHMBAHALTIRL- 157
                                                                                                                                                                                                                                                                      VLGIETSCDETGIAIYDDEKGLLANQLYSQVKLHADYGGVVPELASRDHVRKTVPLIQAA 62
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                                                                                                                                                        LKBSGLTAKD I DAVAYTAGPGLVGALLVGATVGRSLAFAWNVPA I PVHIMEGHLLAPMLB
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                                                                                                                                                                                                                                                                                                                                                                                          23.0%; Score 488.5; DB 2; ilarity 35.2%; Pred. No. 7.8e-32; Conservative 55; Mismatches 148;
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Pred. No. 3.7e-32;
11; Mismatches 143;
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O-sialoglycoprotein endopeptidase (BC 3.4.24.57) - Escherichia coli (strain C;Species: Escherichia coli (c;Species: Bscherichia coli (c;Date: 30-Jun-1988 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004 C;Accession: F65934; D2304; P2304; P2304; P3304; P3304; P4304; P4304; P5304; P5
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A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7 A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: B85967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: ygjD
C;Superfamily: O-sialoglycoprotein endopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-337 <STO>
A;Cross-references: GB:AE005174; NID:g12517643; PIDN:AAG58198.1; GSPDB:GN00145; UWGP:Z44J
A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, B.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Nature 409, 529-533, 2001
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DNPPEPPFVALLVSGGHTQLISVTGIGQYELLGESIDDAAGEAPDKTAKLLGL-DYP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSASGVSPSDLSAIATTIKPGLALSLGVGLSPSLQLVGQLKKPFIPIHHMEAHALTIRL- 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VLGIETSCDDTAAAVVDETGNVLGEAIHSQTEVHLKTGGIVPPAAQQLHRENIQRIVQEA
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                                                                                                                                                      ILSSAADIAATVOHTMACHLVKRTHRAILFCKORDLLPONNAVLVASGGVASNFYIRRAL
                                                                                                                                                                                                                                                        TWSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKGQ 277
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                                                                                                       -- OTRADIARAFEDAVVDTLMIKCKRAL----- DLTGFKR--LVMAGGVSANRTLRAKL
                                                                                                                                                                                                           ---GGPLLSKMAAQGTAGREVFPREMTDREGLDESESGLKTFAANTI----RDNGTDD--
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Potamousis,
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Burland, V.; Riley,

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K-12)

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probable glycoprotease (imported) - Salmonella enterica subsp. enterica serovar Typhi (S.;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AG0892
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Anthors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Residues: 1-337 <ARS.
A;Residues: 1-337 <ARS.
A;Residues: 1-337 <ARS.
A;Cross-references: GB:AL513382; PIDN:CAD07733.1; PID:g16504285; GSPDB:GN00176
C;Genetics: CRY21207
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A;Accession: F65094
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-337 <BLAT>
A;Cross-references: UNIPROT:P05852; GB:AE000388; GB:U00096; NID:g1789441; PIDN:AAC76100.
A;Experimental source: strain K-12, substrain MG1655
A;Experimental source: strain K-12, substrain MG1655
R;Resin, M: Lupski, J.R.; Svec, P.; Godson, G.N.
Gene 51, 149-161, 1987
A;Title: Possible new genes as revealed by molecular analysis of a 5-kb Escherichia coli
A;Reference number: A91573; MUID:87248073; PMID:3297921
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A; Cross-references: GB:M15194; GB:X00773; NID:g14776;
C; Genetics:
A; Gene: ygjb
A; Manap position: 67 min
A; Map position: 67 min
C; Superfamily: O-sialoglycoprotein endopeptidase
C; Keywords: hydrolase; metalloproteinase; zinc
F; 111,115/Binding site: zinc (His) #status predicted
A;Gene: STY3387
C;Superfamily: O-sialoglycoprotein endopeptidase
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A; Molecule type: DNA
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Best Local
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TNKVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECS

ENAPEPPFVALLVSGGHTQLISVTGIGEYLLLGESVDDAAGEAFDKTAKLLGL-DYP---

TMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKGQ

277 178

229

-GGPMLSRMAQQGTVGRFTFPRPMTDRPGLDFSFSGLKTFAANTIRANGDDD-----

LSASGVSPSDLSAIATTIKPGLALSLGVGLSFSLQLVGQLKKPFIPIHHMEAHALTIRL-

VLGIETSCDETGIAVYDDKAGLLANQLYSQVKLHADYGGVVPELASRDHVRKTVPLIQAA

LKEANLSAKDIDAVAYTAGPGLVGALLVGATIGRALAFAWGVPAVPVHHMEGHLLAPMLE

122 157 62

123 158 Ś

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R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
AI0079
                                                                                                                                                                                                                                                                         Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative A;Reference number: AB0001; MUID:21470413; PMID:11586360 A;Accession: AI0079
                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: AI0079
R;Parkhill, J.; Wren
                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable glycoproteinase gcp (imported] - Yersinia
C;Species: Yersinia pestis
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C;Superfamily: O-sialoglycoprotein endopeptidase
                                                                                                                                                                       A;Cross-references: GB:AL590842; C;Genetics:
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A; Residues: 1-337 < KUR>
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                                                  Query Match
Best Local S
Matches 123
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Best Local Similarity
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                                                                       22.8%; Score 483.5; DB 34.6%; Pred. No. 2e-31;
                                                                                                                                                                                            PIDN:CAC89500.1;
                                                    Mismatches 150;
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Search Job ti	DЬ	Ş	뮹
Search completed: February 16, 2005, 13:09:20 Job time : 19.9 secs	279 LADMYQKRGGEVFYARPEFCTDNGAMIAYAGMYRLRSNLNSELSVSVRPRWPL 331	337 LEILTNATOCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDIEGIRYEPKCPL 392	230 QTRADIARAFEDAVVDTLAIKSKRALDQTGFKRLVIAGGVSANQTLRLK 278

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Result
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-MODEL-frame+ p2n.model -DEV=xlh
-Q=/cgn2 1/USPTO_spool/US10649273/runat 14022005 114703 16411/app_query.fasta_1.1429
-Q=/cgn2 1/USPTO_spool/US10649273/runat 14022005 114703 16411/app_query.fasta_1.1429
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10649273 @CGN 1 1 6799 @runat 14022005 114703 16411 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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## ALIGNMENTS

	AUTHORS	REFERENCE	PUBMBD	MEDLINE	JOURNAL		TITLB		AUTHORS	REPERENCE	PUBMED	MEDLINE	JOURNAL	TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION				DEFINITION	LOCUS	AK045669	PRSIT.T 1
Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,	10	11042159	20499374	Genome Res. 10 (10), 1617-1630 (2000)	prepare full-length cDNA libraries for rapid discovery of new genes	Normalization and subtraction of cap-trapper-selected cDNAs to	Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,	N	10349636	99279253	Meth. Bnzymol. 303, 19-44 (1999)	High-efficiency full-length cDNA cloning	Carninci, P. and Hayashizaki, Y.	1	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mus musculus	Mus musculus (house mouse)	HTC; CAP trapper.	AK045669.1 GI:26337528	AK045669	sequence.	PUTATIVE SIALOGLYCOPROTEASE TYPE 2 (Homo sapiens), full insert	full-length enriched library clone:B230219017 product:similar to	ulus adult male corpora quadrigemina cDNA, R	AK045669 2284 bp mRNA linear HTC 03-APR-2004		

CO738006

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PUBMED
REFERENCE
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Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Pax:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,B., Watahiki, Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The FANTOM Consortium and the RIKEN Group Phase I & II Team.
Analysis of the mouse transcriptome of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Please visit c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in
Genomic Sciences Center and Genome Science Laboratory in RIKE
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6 (bases 1 to 2284)
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                  /codon_start=1
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VEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECST
                                                                                                                                                                          /note="unnamed protein product; putative similar to PUTATIVE SIALOGLYCOPROTEASE TYPE 2 sapiens] (SPTR|Q9H4B0, evidence: FASTY, 80%ID,
                                                                                                                                                                                                                                                /strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                     clone="B230219017"
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                                                                                                            Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, B., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system—384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                        Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
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1622 bp mRNA linear HTC 03-APR-2004
Mus musculus 10 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:2610001M19 product:similar to PUTATIVE
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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    FANTOM Consortium
                        The RIKEN Genome Exploration Research Group Phase
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoham Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.jp/) for furti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Group Phase I & II Team.
Analysis of the mouse transcriptome based on of 60,770 full-length cDNAs
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/protein_id="BAB27506.1"
/protein_id="BAB27506.1"
/db_xref="GI:12847276"
/translation="MLMLRRTNGAIPKEPKSKYYGPLRRPSVHPRTLSCHKLYLGIET
SCDDTGAAVVDETGNVLGEALHSQTQVHLKTGGIVPPVAQQLHRENIQRIVEETLSAC
RITPSDLSAIATTIKPGLALSLGVGUSDFLLLGKSLDIAPGDMLDKARRLSLIKHPECST
VEPPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKARRLSLIKHPECST
                                                                                                                                                                                                                                                                                                                                                    /note="unnamed protein product; putative similar to PUTATIVE SIALOGLYCOPROTEASE TYPE 2 sapiens] (SPTR|Q9H4B0, evidence: FASTY, 80%ID,
                                                                        GVDISREVARAAIKVPRLKMAL*
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QI LSSAAD I AAAVQHATACHLAKRTHRA I LFCKQKNLLS PANAVLVVSGGVASNL Y I R
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/clone_Tib="RIKEN full-length enriched mouse
/dev_stage="10 days embryo"
207._.1451
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/db_xref="taxon:10090"
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                   SerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCysHisLeuValLysArg
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                                                                                                 Strausberg, R.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
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Mus musculus O-sialoglycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone IMAGE: 1226118),
                                                                                                                                                                                                                                                                                                                                                                                                            Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                      Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:21040459
                                                                                                                                                                                                                                                                                                                                                                                                                                              (house mouse)
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CE 1 (bases 1 to 1609)

RS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

RS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Altechnl, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Parmer, A.A., Rubin, G. M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carrinci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A.,

Pahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Kzzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Marcello Bento Soares, Ph.D.
cDNA Library Preparation: M. Bento Soares, University of
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                      Submitted (20-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCAGAAGCTGCCATAAAAGTACCGCGATTAAAAATGGCACTT 1448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA linear
endopeptidase-like
frame-shift errors.
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FEATURES

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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov Series: IRAK Plate: 66 Row: e Column: 10 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21312463 This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton,
Madan, Stephanie Rodrigues, Amy Sanchez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA Sequencing by: Institute for Systems http://www.systemsbiology.org
| IGlnGlyValSerAspPheLeuLeuGlyLysSerLeuAspIleAlaProGlyAspMe 200
                                                        SValGluPheProPheLeuValLeuLeuIleSerGlyGlyHisCysLeuLeuAlaLeuVa 180
                                                                                                                                                    sProPheIleProIleHisHisMetGluAlaHisAlaLeuThrIleArgLeuThrAsnLy 160
                                                                                                                                                                                                                           uAlaLeuSerLeuGlyValGlyLeuSerPheSerLeuGlnLeuValGlyGlnLeuLysLy
                                                                                                                                                                                                                                                                           rAlaSerGlyValSerProSerAspLeuSerAlaIleAlaThrThrIleLysProGlyLe 120
                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuGlyGluAlaIleHisSerGlnThrGluValHisLeu-LysThrGlyGlyIleValPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlyIleGluThrSerCysAspAspThrAlaAlaAlaValValAspGluThrGlyAsnVal
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                                                                                                                                                                                                                                                                                                                                                                     oProAlaAlaGlnGlnLeuHisArgGluAsnIleGlnArgIleValGlnGluAlaLeuSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGAATTGAAACCAGCTGTGATGACACAGGAGCGGCTGTGGTGGATGAAACTGGGAATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGCTAATGTTAAGAAGGACAGCAGGAGCTATTCCCAAAGCCCCCAAAGAGTAAAGTTTAT
                                                                                                                                 GCCATTCATCCCGATTCATCACATGGAGGCTCACGCACTGACTATTAGGCTCACCAATAA
                                                                                                                                                                                                        GGCCCTAAGCTTGGGAGTTGGCCTTATCCTTTAGCTTACAGCTAGTAAATCAGTTTAAAAA
                                                                                                                                                                                                                                                                                                                                                     TCCAGTAGCTCAACAACTTCACAGAGAAAATATTCAACGAATAGTAGAAGAAACTCTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                            CTGGGGGAAGCACTCCCAAACTCAGGTTCATCTGAAGT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Thymus gland, mouse"
/clone_lib="Soares_thymus_2NbMT"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/db_mage:1226118"
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1634.00
83.86%
78.80%
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mark Ketteman,
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                               SOURCE
ORGANISM
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KEYWORDS
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                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 870)

11 (hases 1 to 870)

12 (hases 1 to 10)

13 (hases 1 to 10)

14 (hases 1 to 10)

15 (haccontains for the line of Health, Mammalian Gene Collection (MGC)

16 (199)
                                                                                                                                                                                                                                                                                                                                                                                            870 bp AGENCOURT 7790948 NIH_MGC_72 Homo 5', mRNA sequence.
                CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.B. Consortium DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: WGC clone distribution informatifound through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov
plate: LLAM13342 row: l column: 21
                                                                                                                                            Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
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            PheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCys
                                                                    ArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyValAlaSerAsn
                                                                                                          CACACAATGGCATGTCATCTTGTGAAAAGAACACATCGGGCTATTCTGTTTTGTAAGCAG
                                                                                                                                                                GAAGGTATTGAGAAGGGGCAAATCCTGTCTTCAGCAGCAGACATTGCTGCCACAGTACAG
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TTCTATATCCGCAGAGCTCTGGAAATTTTAACAAACGCAACACAGTGCACTTTGGTGTGT
                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MCC_72"
/note="Organ: sKin; Vector: pCMV-SPORT6; Site_1: Not1;
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
/site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life Technologies."
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6065828"
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Enharyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Enharyota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Enharyota; Metazoa; Chordata; Chordata; Homo.

Enhall-length cDNA libraries and normalization

Enhall-length cDNA library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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/cell line="HELA"
/clone lib="HOMO Sapiens HELA CELLS COT 25-NORMALIZED"
/clone lib="HOMO Sapiens HELA CELLS COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
/clone="CS0DK001YE02"
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|mol_type="mRNA"
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Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 922)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
                                                                                        Homo sapiens
                                                                                                            AGENCOURT_8863711 NIH_MGC_18 Homo sapiens cDNA clone 5', maxa sequence.
                                                                                                 Homo sapiens (human)
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Best Local Similarity:
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2603 row: d column: 15
High quality sequence stop: 584.
Location/Qualifiers
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eLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGlyLeuGlnHisVa
                                                                                        MetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGluCys-SerThrMe
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/lab host="DHIOB (phage-resistant)"
/clone_lib="NIH_MGC_18"
/clone_lib="NIH_MGC_18"
/clone_lib="NIH_MGC_18"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
/ECORI, CDNA made by Oligo-dT priming. Directionally cloned into EcoRI/KhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
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RESULT 7
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1 (bases 1 to 701)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM814 row: n column: 09
High quality sequence stop: 701.
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/clome libe"NNH MGC 9"
/clome libe"NNH MGC 9"
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adaptor: GGCACCAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZaP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                 /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:3949640"
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CK982692
CK982692.1 GI:45500672
EST.
1 (bases 1 to 745 Sonstegard, T.S.,
                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                           Bos taurus
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                                      Bovinae; Bos.
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                    (bases 1 to 749)
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     Van
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Bos taurus cDNA clone
                                                        Chordata; Craniata; Vertebrata; Eute Cetartiodactyla; Ruminantia; Pecora;
   Tassell,
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9BOV45_M02 5', mRNA
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     L.X.,
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cora; Bovidae;
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601 324 541 304 481 284 421 264 361 244 301 224 241 204 181 184 121 164 61

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Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim_alt "-trim_fasta. Vector identified
by cross match using options -minmatch 12 -minscore 18
Plate: 45 row: M column: 02
Seq primer: CCCAGTCACGACGTTGTAAAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2004)
Contact: Tad S. Sonstegard
Contact: Tad S. Sonstegard
Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute
Bdlg. 200 Rm2A BARC-East, Beltsville, MD
Tel: 3015048414
Fax: 3015048414
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                 LeuIleSerGlyGlyHisCysLeuLeuAlaLeuValGlnGlyValSerAspPheLeuLeu 188
                                                                                         GluAlaHisAlaLeuThrIleArgLeuThrAsnLysValGluPheProPheLeuValLeu 168
                                                                                                                                                                   SerPheSerLeuGlnLeuValGlyGlnLeuLysLysProPheIleProIleHisHisMet 148
                                                                                                                                                                                                                                           LeuSerAlaIleAlaThrThrIleLysProGlyLeuAlaLeuSerLeuGlyValGlyLeu 128
                                                                                                                                                                                                                                                                                                                   GluAsnIleGlnArgIleValGlnGluAlaLeuSerAlaSerGlyValSerProSerAsp 108
                                                                                                                                                                                                                                                                                                                                                                    ACTGAAGTTCATTTAAAAACAGGTGGGATTATTCCTCCAGTAGCTCAACAGCTTCATAGA
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TIGATTTCTGGAGGTCATTGTCTTTTGGCATTAGTTAGAGGAGTTTCAGATTTTCTTCTT
                                                                        GAGGCTCATGCACTCACTATTAGGTTAACAAATAAGGTAGAATTTCCGTTTTTAGTTCTT
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Location/Qualifiers
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/lab_host="PH10B TI phage resistant"
/clone_lib="BARC 9BOV"
/clone_lib="BARC 9BOV"
/note="Organ: Abomasum; Vector: phgen-1; Site_1: EcoRV;
Site_2: Not1; Equimolar amounts of mRNA extracted from fundic and pyloric abomasums of 18 and 21 week old steers.
Exposure to Ostertagia ostertagi was initiated at 15 weeks of age. fundic and pyloric abomasum"
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/clone="9BOV45_M02"
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/strain="Holstein"
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                                                                                                                                                                                                                                                                                                                                                                                   Laboratory for Environmental Gene Regulation University of Liverpool School of Biological Sciences, The Bioscience Street, Liverpool, United Kingdom, L69 7ZB Tel: +44(0)151-795-4510 Fax: +44(0)151-795-4431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     800 bp mRNA linear EST 29-JUL-2004 S1LH03c19e02f1 squirrel heart library 1 Spermophilus lateralis cDNA clone 19e02 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2004)
Contact: Andrew R. Cossins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Williams,D.R., Gracey,A.Y., Martin,S.L., Hughes,M.A., Li,W., Rogers,J. and Cossins,A.R. Rogers,J. and Cossins, A.R. and Cossins of transcriptional changes during hibernation microarray analysis of transcriptional changes during hibernation in the golden mantled ground squirrel, Spermophilus lateralis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST
                                                                                                                                                                                                                                                                                                                                               Email: cossins@liv.ac.uk
Vector has been trimmed from this EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
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primer: pflc T7 (5'-AATACGACTCACTATAGGG-3')
                                                                                                                                                                                                                                                                   quality sequence stop:
Location/Qualifiers
        /sex="Male & female"
/tissue_type="Heart"
/dev_stage="Adult"
/lab_host="B.coli Electromax DH10B"
/clone_lib="squirrel heart library IT
/note="Vector: pDfC; Site 1: SalI GTCGAG; Site_2: BamHI
GENTCC; Normalized and subtracted cDNA library prepared
from heart of hibernating and summer animals"
                                                                                                                                                                        /db_xref="taxon:76772"
/clone="19e02"
                                                                                                                                                                                                            organism="Spermophilus/mol_type="mRNA"
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Alignment

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1109)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                     BM907988 1109 k
AGENCORT 6707465 NIH_MGC_119
5', mRNA sequence.
EM907988
                                                                                          Homo sapiens (human)
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM12767 row: b column: 07
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Location/Qualifiers
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                                   ProPheIleProIleHisHisMetGluAlaHisAlaLeuThrIleArgLeuThrAsnLys
                                                                          AlaLeuSerLeuGlyValGlyLeuSerPheSerLeuGlnLeuValGlyGlnLeuLysLys
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                    CCATTCATTCCCATTCATCATATGGAGGCTCATGCACTTACTATTAGGTTGACCAATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="NIH MGC_119"
/clone lib="NIH MGC_119"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: ECORV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (ECORV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5744934"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        this is a NIH_MGC Library."
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/lab_host="DH10B"
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Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                  Dept. of Molecular Biosciences, School of Veterinary Medicine University of California, Davis
1311 Haring Hall, One Shields Avenue, Davis, CA 95616, USA Tel: 530 752 0793
Fax: 530 752 4698
Email: mashultz@ucdavis.edu
                                                                                                                                                                                                                                                                                                                                                                                            Shultz, M.A., Zhang, L., Gu, Y.-Z., Baker, G.L., Fannuchi, M.V., Padua, A.M., Gurske, W.A., Morin, D., Penn, S.G., Jovanovich, S. Plopper, C.G. and Buckpitt, A.R. Gene expression analysis in response to lung toxicants: I. Sequencing and microarray development Sequencing and microarray development Am. J. Respir. Cell Mol. Biol. 30 (3), 296-310 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CF114247 765 bp mRNA linear EST 23-JUL-2003 Shultzomica07498 Rat lung airway and parenchyma cDNA libraries Rattus norvegicus cDNA clone NA4935 5', mRNA sequence.
                                                                                                                                                                                                                      Average Phred score is 20 or better. All poor quality 20) and vector/linker sequence has been removed.

High quality sequence stop: 765.

Location/Qualifiers
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CF114247.1 GI:33173962
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         /tissue_type="airway or parenchyma"
/dev stage="adult"
/dev stage="adult"
/clone_lib="Rat lung airway and parenchyma cDNA libraries"
/clone_tib="Organ: lung; Vcctor: pGEW-ilZf(-); Site_1: Eco RI;
Site_2: Not I; mRNA was isolated from microdissected rat
lung airways and parenchyma tissues."
                                                                                                                      /mol type="mRNA"
/strain="Sprague-Dawley"
/db xref="taxon:10116"
/clone="NA4935"
                                                                                                              /sex="male"
                                                                                                                                                                                      organism="Rattus norvegicus"
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hd03d11.y1 Human Retina
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Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A.,
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
Expressed sequence tag analysis of human retina for the NEIBank
Project: Retbindin, an abundant, novel retinal cDNA and alternat
splicing of other retina-preferred gene transcripts
Mol. Vis. 8 (4), 196-204 (2002)
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Plate: 03 row: d column: 11
Seq primer: M13RP1 reverse primer (ABI).
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Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
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                        LysCysGluLysGluGluGlyIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIle
                                                                                                                                                                                                GluHisLeuAlaLysGlnGlyAsnArgPheHisPheAspIleLysProProLeuHisHis
                                                                                                                                                                                                                                                                                       ArgArgLeuSerLeuIleLysHisProGluCysSerThrMetSerGlyGlyLysAlaIle
                                                                                       GCTAAAAATTGTGATTTTTCTTTTACTGGACTTCAACACGTTACTGATAAAATAATAATG
                                                                                                         AlaLysAsnCysAspPheSerPheThrGlyLeuGlnHisValThrAspLysIleIleMet
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301 496 0078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pSPORT1 vector (Life Technologies) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's Instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="Human Retina cDNA (Un-normalized, unamplified): hd/he"
/note="Organ: Bye; Vector: pSPORT1; Neural retina tissue
/note="Organ: Bye; Vector: pSPORT1; Neural retina tissue
was dissected from two 80 year old donors with no observed
eye disease. 100ug of total RNA was used for library
construction. A directionally cloned cDNA library in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="Retina"
/dev_stage="Adult"
/lab_host="EMDH10B"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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University of Edinburgh
Summerhall Square, Edinburgh, EH9 10
Email: j.hopkins@ed.ac.uk
Plate: 04 row: N column: 08
Seq primer: M13reverse
High quality sequence start: 6
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Oa_splbn_04N08_M13reverse Sheep
aries cDNA clone Oa_splbn_04N08
CN823245
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Gossner, A. and Hopkins, J.
Ovine spleen\brain cDNA library
Unpublished (2004)
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CN823245.1 GI:47951314
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Ovis aries (sheep)
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Mammalia; Eutheria;
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(1-414)
                                                                                                                                                                                                                                                  quality sequence start: 6 quality sequence stop: 550. Location/Qualifiers
                                                                                                                                                  /organism="Ovis aries"
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/clone_lib="Sheep spleen\brain_psub_note="Vector: pSport1"
                           1.08e-106
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x CN823245
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                                              l (bases 1 to 661)
Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassell,C.E
Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassell,C.E
Matukumalli,L.K.
Construction and Analysis of a cDNA Library Generated Prom
Intestinal Muscle and Epithelial Tissues of Holstein Cattle
Unpublished (2004)
Contact: Richard G. Baumann
Contact: Richard G. Baumann
                                                                                                                                                                                                                                                                                                                               CK833139
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: rbaumann@anri.barc.usda.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlyLysSerLeuAspIleAlaProGlyAspMetLeuAspLysValAlaArgArgLeuSer
                                                  ARTATTCAACGCATAGTACAAGAAGCTCTCTCTGCCAGTGAAGTCTCTCCCAAGTGAACTC
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                                                                                                                 GCTCATGCACTCACTATTAGGTTAACAAATAAGGTAGAATTTCCGTTTTTAGTTCTTTTG
                                                                                                                                    AlaHisAlaLeuThrIleArgLeuThrAsnLysValGluPheProPheLeuValLeuLeu
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/dev_stage="Lactating, Neonatal"
/lab_hoste="DHIOB TONA"
/lab_hoste="DHIOB TONA"
/clone_lib="BARC 8BOV"
/note="Organ: Intestine; Vector: pCMVSport6.1; Site 1:
Noti; Site 2: EcoRi; Normalized cow cDNA intestinal—
library in pCMVsport6.1, constructed from equimolar mRNA
pools derived from 5 sources, 4 lactating intestinal, 1
neonatal intestinal 4/5 Lactating, Proximal Duodenum,
Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
Duodenum, Jejunum, Distal Ileum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="8BOV_20020"
/sex="Female"
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/strain="Holstein"
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium
CDNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM13213 row: d column: 19
High quality sequence stop: 674.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGENCOURT 7760756 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6016098 5', mENA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; V
Mammalia; Eutheria; Primates; Catarrhini;
1 (bases 1 to 879)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH108 (phage-resistant)"
/clone_lib="NIH MGC_92"
/note="Organ: testis; Vector: pCMV-SpORT6; Site_1: NotI;
/note="Organ: testis; Vector: pCMV-SpORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT_primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type= ".....9606"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
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Search completed: February 16, 2005, 21:04:35 Job time : 4943.95 secs

Copyright

GenCore version (c) 1993 - 2005

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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08blb6 mus musculu
09d0n0 mus musculu
06ayn7 rattus norv
08jfr3 brachydanio
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07q9i8 anopheles g
09vwd6 drosophila
022148 rhizobium m
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GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0008270; F:zinc ion binding; IEA.
GO; GO:0008508; P:proteolysis and peptidolysis; IEA.
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InterPro; IPR009180; Peptidase M22.
InterPro; IPR009180; Peptidase M22; 1.
PIRNF; PIRNF004537; Osialgle pptds; 1.
PIRNFS; PR00789; OSIALOPTASE.
PRODOM; PD002367; Peptidase M22; 1.
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Submitted (CCT-2000) to the EMBL/GenBank/DDBJ
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RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Murakami K., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Ono Y., Takiguchi S., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA Ono Y., Takahashi-Pujii A., Hara H., Tanase T., Nomura Y.,
RA Kamehori K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Yamazaki R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Mutsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein FLJ30879.
Homo sapiens (Human).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Best Local S
Matches 361
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MEROPS; M22.004; -..

GO; GO:0008450; F:O-sialoglycoprotein endopeptidase activity; IEA.

GO; GO:0008233; F:peptidase activity; IEA.

GO; GO:0008270; F:Zinc ion binding; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

InterPro; IPR000905; Peptidase M22.

InterPro; IPR0009180; Peptidase M22.

InterPro; IPR009180; Peptidase M22; 1.

PIRSF; PIRSF004537; Osialglc_pptds; 1.

PRINTS; PR007389; OSIALOPTASE.

PRODOM; PD002367; Peptidase M22; 1.
                                                                                                                     O6PEB4;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse).
STRAIN=CZECH II; TISSIE=Mammary tumor;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Peingold B.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler
                                                                                              Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                       Q6PEB4
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Okumura K., Nagase
Nakai K., Yada T.,
                                                       SEQUENCE FROM N.A.
                                                                              NCBI_TaxID=10090;
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Nagase T., Nomura N., Kikuchi
Ada T., Nakamura Y., Ohara O.,
equencing and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                        PRELIMINARY;
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Pred. No. 8.4e-134;
                                                                                           Craniata; Vertebrata; Buteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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H., Masuho Y., Yamashita R.,
IBogai T., Sugano S.;
of 21,243 full-length human
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Matches
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R GO; GO:0008450; F:O-sialoglycoprotein endopeptidase act
R GO; GO:0008270; F:zinc ion binding; IEA.
R GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
R InterPro; IPR000905; Peptidase M22.
R InterPro; IPR0019180; Pept M22 Osialg1.
R FIREF; PT00814; Peptidase M22; I.
R PIRSF; PTRSF004537; Osialg1c pptds; 1.
R PIRSF; PTRSF004537; Osialg1c pptds; 1.
R PRINTS; PR00789; OSIALOPTASE.
R PRODOM; PD002367; Peptidase M22; 1.
R PTGRPAMs; TIGR00329; gcp; 1.
SEQUENCE 414 AA; 44962 MW; 0418AD93C6FEBCAE CRC64;
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Best Local
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STRAIN-CZECH II; TISSUE-Mammary tumor;
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IMIAWNGI ERLRAGLGILHDIEGIRYEPKCPLGVDISKEVGEASIKVPQLKMBI
                                                                                       QGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIK 240
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Pred. No. 5.8e-133
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RESULT Q8BLB6 ID Q

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**08BTB6** 

PRBLIMINARY;

PRT;

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C. STRAIN-6578LL/G; TISSUE=Corpora quadrigemina;

CA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

A Adachi J., Aizawa K., Akimura T., Harakawa T., Hashizume W.,

Pukuda S., Furuno M., Hanagaki T., Haraka T., Hiraoka T.,

A Hayashida K., Hayatsu N., Hiraoka T., Hiraoka T.,

A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Nakamura M.,

A Katoh H., Kawai J., Kojima Y., Kondo M., Ohsato N., Okazaki Y.,

A Mishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

A Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T.,

A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T.,

A Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,

Euri Yuki C. (UUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
MEDINE=20530913; PubMed=11076861; DOI-10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA) system—384-format
sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771(2000).
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length
enriched library, clone:B230219017 product:similar to PUTATIVE
SIALOGLYCOPROTEASE TYPE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10:1617-1630(2000).
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[3]
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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TISSUE=Corpora
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"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
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Nature 409:685-690(2001).
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R MGD; MGI:1919335; Osgepl1.

R GG; GO:0008450; F:0-sialoglycoprotein endopeptidase activity; IEA.

R GG; GO:0008233; F:peptidase activity; IEA.

DR GG; GO:0008270; F:zinc ion binding; IEA.

DR GG; GO:00068270; F:zinc ion binding; IEA.

DR GG; GO:00068270; F:zinc ion binding; IEA.

DR InterPro; IPR000905; Peptidase M22.

DR InterPro; IPR000905; Peptidase M22.

DR InterPro; IPR000905; Peptidase M22.

DR Pfam; PP00814; Peptidaee M22; 1.

DR PIRSF; PIRSF004537; Osialglc_pptds; 1.

DR PIRSF; PR00789; OSIALOPTASE.

DR ProDom; PD002367; Peptidase M22; 1.

DR PTOR; PD002367; Peptidase M22; 1.
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Best Local S
Matches 352
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Q9DONO;
01-JUN-2001
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01-JUN-2001 (TrEMELrel. 17, Last sequence update)
01-MAR-2004 (TrEMELrel. 26, Last annotation update)
Mus musculus 10 days embryo whole body cDNA, RIKEN
enriched library, clone:2610001M19 product:similar
SIALOGLYCOPROTEASE TYPE 2.
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SEQUENCE
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                    Name=Osgepl1;
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                                                                                                                                                                                                                                            Chordata;
Rodentia;
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85.0%; Pred. No. 2.4e-132;
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Sciurognathi; Muridae;
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to PUTATIVE
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SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE=Whole body;
STRAIN-C57BL/6J; pubMed=10349636;
MEDLINE=99279253; pubMed=10349636;
Carninci P., Hayashizaki Y.;
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Enzymol.

303:19-44 (1999)

cloning.";

DOI=10.1016/S0076-6879(99)03004-9;

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Query Match
Best Local S
Matches 351
                                                                                                                                                                                                                                                                                                                                                                                            Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
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Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.
Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                 Protease.
SEQUENCE
                                                                                                                                       InterPro; IPR000905; Peptidase M22.
InterPro; IPR009180; Pept M22 Osialg1.
Pfam; PF00814; Peptidase M22; 1.
PIRSF; PIRSF004537; Osialg1c pptds; 1.
PRINTS; PR00789; OSIALOPTASE.
PRODOm; PD002367; Peptidase M22; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., Watahiki M., Yokazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-C57BL/6J; TISSUE=Whole body;
MEDLINE=20499374; PubMed=1102501=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., It
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new ge
Genome Res. 10:1617-1630(2000).
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                                                                                                                        TIGRFAMs; TIGR00329;
                                                                                                                                                                                                                                                                                                                                       MEROPS; M22.004; -.
MGD; MGI:1919335; O8gepl1.
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MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDMAs."; Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The FANTOM Consortium
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STRAIN=C57BL/6J; TISSUE=Whole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection.";
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                                                                                                                                                                                                                                                         GO:0008450; P:O-Sialoglycoprotein endopeptidase activity; IEA.
GO:0008233; P:peptidase activity; IEA.
GO:0008270; P:zinc ion binding; IEA.
GO:0006508; P:proteolysis and peptidolysis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                  AK011265; BAB27506.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               409:685-690(2001).
                      Similarity
                                                                                 414
    Conservative
                                                                                 Ş.
                                                                                 44999 MW;
                    85.6%;
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    23;
Score 1819; Di
Prod. No. 9.9e-
23; Mismatches
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                                                                               999BC689944DDB24 CRC64;
                  9; DB 2;
9.9e-132;
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                                                                                                                                                                                                                                          RX PubMed-12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschal S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschanko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haigh C.,
RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Kzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.B.,
RA Alnes S. J. Marra M.A.
Director MGC Project;

$\text{Submitted (AUG-2004) to the EMBL/GenBank/DUBJ databa EMBL; BC078974 AAAH3974.1; -.

$\text{CO:0008450} \cdot \text{F:O-sialoglycoprotein endopeptidase GO; GO:0008270; F:\text{F:inc ion binding; IEA.}

$\text{GO: GO:0006508; P:proteolysis and peptidolysis; IEA.}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein (Fragment).
Rattus norvegicus (Rat).
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25-OCT-2004 (TrEMBLrel.
25-OCT-2004 (TrEMBLrel.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                    TISSUE=Testis;
                                                                                                                                                                                                               "Generation and initial analysis of more than 15,000
                                                                                                                                                                                                                                  Jones S.J., Marra M.A.;
                                                                                                                                                                       mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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28, Last sequence update;
28, Last annotation updat
                                                                            ជាចារ់/Genbank/ប៊ីបិទីស៊ី databases
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                                         activity;
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Best Local :
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InterPro; IPR002016; Peroxidase.
Pfam; PP00814; Peptidase_M22; 1.
PIRSF; PIRSF004537; Osialg1c_pptds; 1.
PRINTS; PR00799; OSIALOPTASE.
PRODOm; PD002367; Peptidase_M22; 1.
TIGRPAMs; TIGR00329; gcp; 1.
PROSITE; PS00435; PEROXIDASE_1; UNKNOWN_1.
Babbage A.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AL591593; CAD43471.1; -.

MEROPS; M22.004; -.

GO; GO:0008450; F:O-sialoglycoprotein endopeptidase activity; GO; GO:0008233; F:peptidase activity; IEA.

GO; GO:0008233; F:peptidase and peptidolysis; IEA.

GO; GO:0008270; F:Zinc ion binding; IEA.

GO; GO:0008270; F:Zinc ion binding; IEA.

InterPro; IPR000905; Peptidase M22.

InterPro; IPR000905; Peptidase M22.

InterPro; IPR000905; Peptidase M22.

InterPro; IPR000180; Peptidase M22.
                                                                                                                                                                                                                                                                                                                                     Q8JFW3;
                                                                                                                                                                                                                                                              01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation updat
SI:dZ211013.4 (Novel glycoprotease).
Name=dZ72B14.6;
                                                                                                                                                                                                       Brachydanio rerio (Zebrafish) (Danio rerio).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniform
Cyprinidae; Danio.
                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                         NCBI_TaxID=7955;
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50799 MW; 474E18B1959B8AC0 CRC64;
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Best Local S
Matches 242
                    Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases
EMBL; AL672217; CAD43443.1; -.

MEROPS; M22.004; -.

GO; GO:0008450; F:O-sialoglycoprotein endopeptidase act
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0008279; F:zinc ion binding; IEA.
GO; GO:0008508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR000905; Peptidase M22.
InterPro; IPR001905; Peptidase M22.
InterPro; IPR001905; Peptidase M22.
InterPro; IPR001905; Peptidase M22; I.
PIRSF; PIRSF004537; Osialglc Dptds; 1.
PIRSF; PIRSF004537; Osialglc Dptds; 1.

PRONINTS; PR001939; OSIALOPTASE.
ProDom; PD002167; Peptidase_M22; 1.

TIGRFAMS; TIGR00329; gcp; 1.
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PRINTS; PR00789; OSIALOPTASE.
ProDom; PD002367; Peptidase_M22; 1.
TIGRPAMs; TIGR00329; gcp; 1.
Protease.
SEQUENCE 404 AA; 43956 MW; 3A6B1
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sec
01-MAR-2004 (TrEMBLrel. 26, Last and
SI:dZ72B14.6 (Novel glycoprotease).
                                                                                                                                                                                                                                                  Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                             Q8JFR7
                                                                                                                                                                                                                                                                                                  Name=SI:dZ72B14.6;
   SEQUENCE
               Protease
                                                                                                                                                                                                    Clark G
                                                                                                                                                                                                                SEQUENCE FROM N.A.
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; Craniata; Vertebrata; Euteleostomi; Teleostei; Ostariophysi; Cypriniform
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Pred. No. 1.9e-90
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   6FE98653A651860F CRC64;
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Query Match
Best Local Sir
Matches 165;
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Best Local Similarity
Matches 241; Conserv
                                                                                                                          TIGRFAMS;
                                                                                                                                                                 GO; GO:0008450; F:O-sialoglycoprotein endopeptidase activity; GO; GO:0008270; F:zinc ion binding; IEA.
GO:0008508; F:proteolysis and peptidolysis; IEA.
InterPro; IPR000905; Peptidase M22.
InterPro; IPR009180; Peptidase M22.
Pfam; PP00814; Peptidase M22; 1.
PIRSF; PR098137; Osialglc.pptds; 1.
PRINTS; PR00789; OSIALOPTASE.
PRODOM; PD002367; Peptidase M22; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry v
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Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Metazoa; Arthropoda; Nematocera; Culicoidea; Anopheles.
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01-MAR-2004 (TrEMBLrel.
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Name=agCG46164; ORFNames=ENSANGG00000007922;
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; AAAB01008900; EAA09387.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STWSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIHPLDEPETVLLVSGGHSLLALAKGIDEFLLLGQTLDEAAGDTLDKIARRLSLRNHPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EALNRSAIEPSELTAVATTVKPGLALSLGIGLDYSLKFVRQHQKPFIFIHIMEAHALTVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TSEVKEAAIKVPKLKL
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                                                                                                                                                    TIGR00329;
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                                                                                                MW;
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  68;
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Last annotation update)
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                    Score 772.5; DB 2
Pred. No. 4.2e-51;
                                                                                                  CC9426723D3FD4F1 CRC64;
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           401
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                                            DB 2;
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entry which
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RA Adams M.D., Celniker S.B., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.B., Fichards S.A., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Hann K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Gabor G.L.,
RA Bril J.F., Agbayani A., An H.J., Andrews Pfannkoch C.R., Baldwin D.,
RA Beeson K.Y., Benson P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benson P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport J.B., Davies P.,
RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K., Boup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houtk J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Kimmel B.B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Leviteky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson C.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
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Q9VWD6;
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01-MAY-2000 (TrEMBLrel. 1
01-MAR-2004 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORFNames=CG14231;
Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=10731132; DOI=10.1126/science.287.5461.2185;
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Query Match
Best Local Similarity
Matches 156; Conserv
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FlyBase; FBgn0031060; CG14231.
GO; GO:0008450; F:O-sialoglycoprotein end GO; GO:0008270; F:Zinc ion binding; IEA.
GO; GO:0008270; F:Zinc ion binding; IEA.
GO; GO:0008508; P:proteolysis and peptide InterPro; IPR009105; Peptidase M22.
InterPro; IPR009180; Peptidase M22; I.
Pfam; PF00814; Peptidase M22; 1.
PIRSF; PIRSF004537; Osialglc_pptds; 1.
PRINTS; PR00789; OSIALOPTASE.
PRODOM; PD002367; Peptidase M22; 1.
TIGRFAMS; TIGR00339; gcp; 1.
SEQUENCE 409 AA; 45328 MW; 9797F66E7I
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MEDLINE=22426065; PubMed=12537568;

MEDLINE=22426065; PubMed=2 D.A., Kronmiller B., Carlson J.W., Halpern A
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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P.,
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Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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MEDLINE=22426070; PubMed=12537573;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lewis S.E.;
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Score 714.5; DB 2
Pred. No. 1.3e-46;
0; Mismatches 140
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140;
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1D 02214
AC 02214
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Epermatophyta; Magnoliophyta; eudicotyledons; core en eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Submitted
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01-JAN-1998 (TrEMBLrel. 05,
01-JUN-2002 (TrEMBLrel. 21,
05-JUL-2004 (TrEMBLrel. 27,
                       YAMAGA K., BANH J., Chan M.M.
Yamada K., Banh J., Chan M.M.
Deng J.M., Goldemith A.D., Le
Tang C., Toriumi M., Wu H.C.,
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1 K., Adamska I.;
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  Lee J.M., Onodera C.S., Quach H.L.,
C., Yamamura Y., Yu G., Bowser L.,
k R., Hayashizaki Y., Ishida J., Jon
                                                                                                                                          EMBL/GenBank/DDBJ databases
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Last annotation updat
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                                                                Chang C.H.,
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R., Adams
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Ecker J.R.,
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Best Local S
Matches 154
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Submitted (JUN-2002) to the EMBL
EMBL; AC002387; ALM82636.2; -
EMBL; AY0243387; ALM00530.1; -
EMBL; AY063864; AAL36220.1; -
EMBL; AY117283; AAM51358.1; -
PIR; E84888; E84888.
                                                                                                                    O73H71; PRELIMINARY; PRT; 335 AA.
Q73H71; O5-JUL-2004 (TrEMBLrel. 27, Created)
O5-JUL-2004 (TrEMBLrel. 27, Last sequence update)
O5-JUL-2004 (TrEMBLrel. 27, Last annotation updat
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SEQUENCE
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Miranda M.,
                                            Wolbachia pipientis wMel.
Wolbachia pipientis wMel.
Bacteria; Proteobacteria; Alphaproteobacteria;
                                                                                          Peptidase, M22 family protein.
OrderedLocusNames=WD0699;
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GO; GO:0008270; F:zinc ion binding; IEA.
GO; GO:00085270; P:zinc ion binding; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR000905; Peptidase M22.
InterPro; IPR000905; Peptidase M22.
InterPro; IPR009180; Pept M22 Osialgl.
Pfam; PP00814; Peptidase M22; 1.
PIRSF; PIRSF004537; Osialglc_pptds; 1.
PRINTS; PR00789; OSIALOPTASE.
PRODOM; PD002367; Peptidase_M22; 1.
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 SEQUENCE FROM N.A.
PubMed=15024419;
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Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai
Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.
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                                                                   Rickettsiales;
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Davis R.W., Ecker
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Ecker J.R.,
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DB PROBA
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GO; GO:0008270; F:zinc ion binding; IEA.
GO; GO:0006270; F:zinc ion binding; IEA.
GO; GO:0006508; P:proteclysis and peptidolysis; IEA.
InterPro; IPR00905; Peptidase M22.
InterPro; IPR009180; Pept M22_Osialg1.
Ffam; PF00814; Peptidase M22; 1.
PIRSF; PIRSF004537; Osialg1c_pptds; 1.
PRINTS; PR00789; OSIALOPTASE.
ProDom; PD002367; Peptidase M22; 1.
TIGRFAMS; TIGR00329; gcp; 1.
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Q92LH8;
Q92LH8;
Q1-DEC-2001 (TrEMBLrel. 19, Cre
01-DEC-2001 (TrEMBLrel. 19, Lau
01-MAR-2004 (TrEMBLrel. 26, Lau
PROBABLE O-SIAJOGI/COPROTEIN EI
PROBABLE O-SIAJOGI/COPROTEIN EI
PROBABLE O-SIAJOGI/COPROTEIN EI
ORFNames=SMC03230;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLOS Biol. 2:327-341(2004).
EMBL; AE017258; AAS14395.1; -.
TIGR; WD0699; -.
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36.3%; Pred. No. 3.6e
:ive 68; Mismatches
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MEDLINE=21396507; PubMed=11481430; DOI=10.1073/pnas.161294398; Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J. Botetard P., Becker A., Boutry M., Cadieu B., Dreano S., Gloux S., Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,

SEQUENCE FRO

FROM

N.A.

NCBI\_TaxID=382;

Rhizobium meliloti (Sinorhizobium meliloti). Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobialo Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium

Rhizobiales;

Last sequence update)
Last annotation updat
N ENDOPEPTIDASE (EC 3.

n\_update) (EC 3.4.24.57).

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Q98EIG
ID Q98EI
AC Q98EI
DT 01-0C
DT 01-0C
DT 01-MA
DE 0-sia
GN 0rder
CS Rhizo
OC Bacte
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CX NCBI
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Renard C.,
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GO; GO:0008476; F:O-sialoglycoprotein endopeptidase activity;
GO; GO:0008270; F:zinc ion binding; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR000905; Peptidase M22.
InterPro; IPR00180; Pept M22 Gislalgl.
Pfam; PF00814; Peptidase M22; 1.
PIRSF; PROFF004537; Osialglc pptds; 1.
PRINTS; PRO0789; OSIALOPTASE.
ProDom; PD002367; Peptidase M22; 1.
TIGREAMS; TIGR00329; gcp; 1.
                                                                                                                                                                                                                                                                                                                                          01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation updat
0-sialoglycoprotein endopeptidase (Gcp).
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                                                                               SEQUENCE FROM N.A.
STRAIN-MAFF303099;
MEDLINE-21082930; PubMed=11214968;
  Kaneko T., Nakamura Y., Sato S., Asam
Watanabe A., Idesawa K., Ishikawa A.,
Kishida Y., Kiyokawa C., Kohara M., M
                                                                                                                                                                                                                                      Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                           Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria;
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Pred. No. 1.9e-35;
77; Mismatches 133; Indels 47;
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                                Asamizu E., Kato T., Sasam
a A., Kawashima K., Kimura
     Matsumoto
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EMBL; AP003003 BAB55032.; -...

GO; GO:0008450; F:O-sialoglycoprotein endopeptidase act

GO; GO:0008270; F:zinc ion binding; IEA.

InterPro; IPR000905; Peptidase M22.

InterPro; IPR000905; Peptidase M22.

InterPro; IPR000905; Peptidase M22.

InterPro; IPR000905; Peptidase M22.

INTERPRO; IPR000905; Peptidase M22; 1.

PIRSF; PIRSF004537; Osialglc_pptds; 1.

PIRSF; PIRSF004537; Osialglc_pptds; 1.

PIRSF; PIRSF004537; Peptidase M22; 1.

PIRSF; PIRSF004537; Osialglc_pptds; 1.

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PIRSF; PIRSF004537; Osialglc_pptds; 1.
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Search completed: Pebruary 16, 2005, 13:08:38 Job time: 79.2 secs

Copyright

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

RESULT 1 ABG96487

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Metalloprotease; MP-1; immune disorder; glutamate transport; cancer; motor neuron disorder; amyotrophic lateral sclerosis; ALS; diabetes; reproductive disorder; kleinfelter's syndrome; germinal cell aplasia; genital wart; metabolic disorder; premature puberty; Kallman syndrome; Cushing's syndrome; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; Huntington's disease; Tourette syndrome; sepsis; liver disease; renal disease; munune disorder; rheumatoid arthritis; acquired immunodeficiency syndrome; AIDS; pulmonary disease; pneumonia; emphysema; cystic fibrosis; vascular disorder; inflammatory disorder;
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Homo sapiens.
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WO200272751-A2

19-SEP-2002.

05-FEB-2002; 2002WO-US003353.

05-FEB-2001; 10-APR-2001; 2001US-0266518P. 2001US-0282814P.

(BRIM ) BRISTOL-MYERS SQUIBB CO.

Peder J, Nelson TC, ۳,

Duclos

Krystek

WPI; 2002-723329/78. N-PSDB; ABS76639.

Chen

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New isolated nucleic acid encoding MP-1 protein, useful for preventing, treating, or ameliorating diseases associated with aberrant metalloproteinase activity, e.g. immune, metabolic, inflammatory and neurological disorders. neurological

Claim 5; Page 29; 473pp; English.

The invention describes an isolated nucleic acid molecule (I) encoding a metalloprotease (MP-1). (I) is useful for preventing, treating, or

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Best Local S
Matches 267
                                                                                                                                                                                                                                                                                                                                                                                                                                        motor neuron disorder; amyotrophic lateral sclerosis; ALS; diabetes; reproductive disorder; Kleinfelter's syndrome; germinal cell aplasia; genital wart; metabolic disorder; premature puberty; Kallman syndrome; Cushing's syndrome; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; Huntington's disease; Tourette syndrome; sepsis; liver disease; renal disease; immune disorder; rheumatoid arthritis; acquired immunodeficiency syndrome; AIDS; pulmonary disease; pneumonia; emphysema; Cystic fibrosis; vascular disorder; inflammatory disorder; neurological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human metalloprotease MP1.
    05-FEB-2001; 2001US-0266518P
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Pred. No. 1.4e-147;
; Mismatches 0;
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RESULT 3
ABB05481
ID ABB0
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AC ABB0
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DT 19-A
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DE Huma
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KW Huma

19-APR-2002 ABB05481;

(first entry)

ABB05481 standard; protein;

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Human; O-sialoglycoproteinase-like

protein; OSGPLP; enzyme.

Human O-sialoglycoproteinase-like protein SEQ ID

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention describes an isolated nucleic acid molecule (I) encoding a CC metalloprotease (MP-1). (I) is useful for preventing, treating, or ametalloprotease (MP-1). (I) is useful for preventing, treating, or cameliorating a medical condition, particularly an immune disorder, and cC ameliorating a medical condition, particularly an immune disorder, and cC condition. The compositions and methods are also useful for diagnosing, treating, treating, ameliorating and/or treating disorders (CC condition, treating, ameliorating and/or treating disorders (CC disorders (e.g. Kleinfelter's syndrome, genital warts, or germinal cell (CC disorders (e.g. Kleinfelter's syndrome, genital warts, or germinal cell (CC aplasia), metabolic disorders (e.g. premature puberty, Kallman syndrome, CC or consing's syndrome), neurodegenerative disease (Alzheimer's disease, Huntington's disease or Tourette syndrome), liver (CC parkinson's disease, Huntington's disease or Tourette syndrome), liver (CC arepsie), pulmonary diseases (e.g. pneumonia, emphysema or cystic (cc fibrosis) and vascular, inflammatory and neurological disorders (e.g. Alzheimer's disease or Parkinson's disease). This is the amino acid
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid encoding MP-1 protein, useful for preventing, treating, or ameliorating diseases associated with aberrant metalloproteinase activity, e.g. immune, metabolic, inflammatory and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 414 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence of a metalloprotease MP1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; Fig 1A-C; 473pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-APR-2001; 2001US-0282814P
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                        PKCPLGVDISKEVGEASIKVPQLKMBI 267
                                                                                                       ASNFYIRRALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDIEGIRYE
                                                                                                                                                                                           EKEEGIEKGQILSSAADIAATVQHTWACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGV 180
                                                                                                                                                                                                                                                       LSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKK 267
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                                                                                                                                                                   EKEEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGV
PKCPLGVDISKEVGEASIKVPQLKMEI 414
                                                                                 ASNFYIRRALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDIEGIRYE
                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1385; DB 5; milarity 100.0%; Pred. No. 2.8e-147; Conservative 0; Mismatches 0;
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Homo sapiens

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Best Local S
Matches 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present, sequence represents human O-sialoglycoproteinase-like protein (OSGPLP). The present invention also describes: (1) the preparation of the OSGPLP protein; (2) applying the OSGPLP protein in diagnosis; (3) the prevention and/or treatment of related diseases; (4) utilising the OSGPLP protein in screening its agonist, excitomotor and inhibitor and preparing an antibody against the OSGPLP protein, and (5) the use of the OSGPLP polynucleotide sequences, proteins, agonists, excitomotors, inhibitors and antibodies in treating diseases related to the abnormal OSGPLP gene and in preparing the medicine composite for the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O-sialogycoproteinase-like for diagnosing, preventing
                                       Cytostatic; antiarteriosclerotic; anti-HIV; antiallergic;
                                                                                           01-MAY-2003
                                                                                                                                                 ABJ26654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 30-31 (Disclosure); 38pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-APR-2000; 2000CN-00106834
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                                                                                                                                                                                                                                                                                                                                                                                                                              h 100.0%; Score 1385; DB 5;
Similarity 100.0%; Pred. No. 2.8e-147;
67; Conservative 0; Mismatches 0;
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                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                     ASNFYIRRALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDIEGIRYE
                                                                                                                                                                                                                  PKCPLGVDISKEVGEASIKVPQLKMEI 414
                                                                                                                                                                                                                                 PKCPLGVDISKEVGEASIKVPQLKMEI 267
                                                                                                                                                                                                                                                                      ASNFYIRRALBILTNATOCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDIEGIRYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      414 AA;
                                                                                           (first entry)
                                                                 modification + maintenance molecule protein
                                                                                                                                                protein; 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein and encoding and treating related
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                                         anticonvulsant;
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cerebroprotective; antiparkinsonian; nootropic; antiinflammatory; antiulcer; hepatotropic; gynaecological; antibacterial; virucide; protozoacide; antiparasitic; cell proliferative disease; PMOD;

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MEAHALTIRLTNKVEPPPLVLLISGGHCLLALVQGVSDPLLLGKSLDIAPGDMLDKVARR

Ouery Match Best Local Similarity Matches 267; Conserv

100.0%; ilarity 100.0%; Conservative 0;

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Score 1305; DB 6; Pred. No. 2.8e-147; ; Mismatches 0;

rength

0;

Gaps

Sequence

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The invention relates to an isolated polypeptide comprising: any of 28 sequences of 48-1256 amino acids; a natural amino acid sequence at least CC 90% identical to the 28 amino acids sequences, 94% identical to a sequence of 703 or 267 amino acids, 96% identical to a sequence of 414 amino acids, or 97% identical to a sequence of 242 amino acids, all given in CC the specification; or a biologically active or immunogenic fragment of CC the isolated polypeptide. The polypeptides and polymucleotides are useful in diagnosing, treating and preventing diseases or conditions associated with the decreased expression of protein modification and maintenance CC molecules (PMOD), such as cell proliferative diseases (e.g. AIDS, CC allergies), neurological disorders (e.g. stroke, Parkinson's disease, epilepsy), gastrointestinal (e.g. ulcer, cirrhosis), reproductive (e.g. cendenctriosis), developmental (e.g. ulcer, cirrhosis), reproductive (e.g. cendenctriosis), developmental, vesicle trafficking disorders, and CC infections (e.g. bacterial, viral, parasitic, protozoal). These are also useful in assessing the effects of exogenous compounds on the expression of mucleic acid and amino acid sequences of PMOD. The PMOD or its Cragments are useful in screening compounds for effectiveness as agonist or antagonist of the polypeptides, or in altering the expression of the ctarget polynucleotide and compounds that specifically bind to or modulate the activity of the polypeptide. The microarray is useful in monitoring of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-JUN-2001; 2001US-0300508P.
06-JUL-2001; 2001US-0303445P.
13-JUL-2001; 2001US-0305405P.
09-AUG-2001; 2001US-0311442P.
24-AUG-2001; 2001US-0314821P.
29-AUG-2001; 2001US-0315992P.
03-MAY-2002; 2002US-0378205P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gandhi AR, K
Warren BA, I
Forsythe IJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated human PMOD polypeptide and polynucleotide, useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant PMOD expression, e.g. cancer, AIDS, atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thangavelu K, Gietze Walia NK, Mason PM, Elliott VS, Luo W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein modification and maintenance molecule; immunogenic fragment; cancer; autoimmune; inflammatory disease; neurological disorder; gastrointestinal; developmental; vesicle trafficking disorder; infection; protein-protein interaction; drug-target interaction; gene expression profile; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 63; Page 182-183; 225pp; English.
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N-PSDB; ABT23207.
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Ison CH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kable AE, Swarnakar A, Hafalia AJA, Tran B, Duggar Ison CH, Honchell CD, Nguyen DB, Lu DAM, Lee EA, Barroso I, Ramkumar J, Griffin JA, Li JX, Yang G, Gietzen KJ, Ding L, Baughn MR, Borowsky ML, Yac Iason PM, Gururajan R, Lee S, Becha SD, Lee SY, Thuo W, Sprague WW, Tang YT, Lu Y, Zebarjadian Y;
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se EA, Y
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L, Yao MG;
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7TM; glycoprotease; immune disorder; IgA deficiency; allergy; arrhythmia; rheumatoid arthritis; diabetes; atherosclerosis; cardiovascular disorder; hypertension; ischaemic heart disease; obesity; myocardial infarction; endothelial cell disorder; Grave's disease; psoriasis; brain disorder; Parkinson's disease; Alzheimer's disease; hematopoietic disorder; cerebral oedema; metabolic disorder; liver disorder; platelet disorder; chromosome mapping; tissue typing; gene therapy; neuroprotective; cytostatic; anorectic; cardiant; haemóstatic.
           08-NOV-2001; 2001WO-US051427
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                                                                                                                                                                                                                                                                                                                                                                                                                        Human glycoprotease 28472 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE29234 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASNFYIRRALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDIEGIRYE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PKCPLGVDISKEVGEASIKVPQLKMEI 267
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                                                                                                                                                                                                                                                          /note= "Non-transmembrane domain; N-terminal cytoplasmic domain"
                                                                                                                                                                                                                               metalloprotease
                                                                                                                                                                                          133. .164
                                                                                                       note=
                                                                                                                                                                                                  109. .132
/note= "Transmembrane
                                                                                                                                                                                                                             /note= "Endopeptidase O-sialoglycoprotein hydrolase
metalloprotease zinc glycoprotease sialoglycoprotease
                                                                                                                                                                                                                                                                                      ocation/Qualifiers
                                                                                    note= "Non-transmembrane domain"
                                                                                                                                            not e=
                                                                                                                                                               note= "Glycoprotease
                                                                                                                                                                                 note= "Non-transmembrane domain;
                                                                                                                        note= "Non-transmembrane domain; cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein;
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                                                                                                                  . 333
                                                                                                                                   .316
                                                                                                                                                     .189
                                                                                                                                                                         . 152
                                                                            .414
                                                                                                                                            "Transmembrane domain"
                                                                                                       "Transmembrane
                                                                 "Sialoglycoprotease type domain"
                                                                                                                                                                                                                                                                                                                                                                                                    seven transmembrane domain receptor; cancer;
                                                                                                                                                               domain"
                                                                                                                                                                                 non-cytoplasmic loop'
                                                                                                                         domain"
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                                               standard;
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The present invention relates to novel 38650, 28472, 5495, 65507, 81588 CC or 14354 nucleic acid molecules which encode adenosine deaminase, glyco-cc protease or seven transmembrane domain (77M) receptor family members. CC Sequences of the invention are useful in diagnosing and treating cancer or aberrant cellular proliferation and/or differentiation (e.g. colon or CC lung cancer), immune disorders (e.g. selective IgA deficiency, rheumatoid CC arthritis, diabetes, allergy), heart or cardiovascular disorders (e.g., hypertension, atherosclerosis, arrhythmias, ischaemic heart disease, CC myocardial infarction, thrombus including endothelial cell disorders (e.g., gsoriassis, Grave's disease), haematopoletic disorders, brain CC disorders (e.g. cerebral oedema, Parkinson's or Alzheimer's disease), CC gain and metabolic disorders (e.g. obesity), liver disorders or platelet CC disorders. They are also useful in screening assays, predictive medicine (e.g. diagnostic assays, propostic and therapeutic methods. The cultical cacids may also be used in chromosome mapping, tissue typing and CC canso in gene therapy. The present sequences of the invention are calso used in gene therapy. The present sequence is human glycoprotease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Matches 260;
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08-NOV-2000; 2000US-0246772P.
15-NOV-2000; 2000US-0249185P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 414 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in pharmacogenomics.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                           ASNFYIRRALBILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDIEGIRYE 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEAHALTIRLTNKVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARR
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PKCPLGVDISKEVGEASIKVPQLKMEI 267
                                                                  ASNFYIRRALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDIEGIRYE
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Pred. No. 4.3e-143;
3; Mismatches 4;
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(first entry)

protein;

Cancer; aberrant Novel human

cell proliferation; aberrant cell differentiation;

glycoprotease 28472.

breast cancer; ovarian cancer; prostate cancer; colon cancer; lung cancer; immune disorder; heart disorder; cardiovascular disorder; endothelial disorder; hematopoietic disorder; blood vessel disorder; brain disorder; pain; metabolic disorder; liver disorder; diabetes; platelet disorder; carcinoma; sarcoma; leukaemia; Hodgkin's disease; autoimmune disorder; hypertension, atherosclerosis; heart failure; myocardial infarction; ischaemic heart disease; Crohn's disease; grave's disease; Kawasaki syndrome; Raynaud's disease; aneurysm; cerebral ischaemia; peripheral neuropathy; Alzheimer's disease; enzyme.

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CC 14354 nucleic acid molecules (I) and their encoded polypeptides (II). The CC 38650 nucleic acid molecule comprises a sequence encoding adenosine CC deaminase. The 28472 nucleic acid molecule comprises a sequence encoding adenosine CC deaminase. The 28472 nucleic acid molecule comprises a sequence encoding CC a human glycoprotease. The 5495, 65507, 81588 and 14354 comprises CC sequences that encode a human seven transmembrane domain (7TM). The CC sequences are useful for diagnosing, preventing or treating a subject CC with or at risk of developing a disorder, e.g. cancer or aberrant CC cellular proliferation and/or differentiation (e.g. breast, ovarian, CC prostate, colon or lung cancer), immune disorders, heart disorders, cardiovascular disorders, endothelial disorders, heart disorders, CC liver disorders or platelet disorders, pain and metabolic disorders, CC liver disorders or platelet disorders. These disorders include carcinoma, sarcoma, leukaemia, Hodgkin's disease, autoimmune disorders, Kawasaki CC syndrome, Raynand's disease, Crohn's disease, Grave's disease, Kawasaki CC syndrome, Raynand's disease, aneurysm, cerebral ischaemia, peripheral neuropathy, Alzheimer's disease, Parkinson's disease, anorexia nervosa, CC cachexia or diabetes. This is the amino acid sequence of the novel human
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Matches 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New adenosine deaminase, glycoprotease and seven transmembrane domain nucleic acids and polypeptides, designated 38650, 28472, 5495, 65507, 81588 and 14354, useful for treating e.g. leukemias, Hodgkin's disease
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08-NOV-2000; 2000US-0246772P.
15-NOV-2000; 2000US-0249185P.
                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Fig 8A-B; 178pp; English
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N-PSDB; ABS57020.
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                   Local Similarity
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   Conservative
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138. .152
/label= Glycoproteas
                 97.3%;
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Score 1348; DB 6; Length 414; Pred. No. 4.3e-143; Indels 3; Mismatches 4; Indels
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disease or
   Gaps
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MEAHALTIRLTNKVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARR 60

The invention relates to an isolated 38650 (encoding adenosine deaminase), 28472 (encoding a glycoprotease), 5495 (encoding a 7 transmembrane receptor), 65507, 81588 or 14354 nucleic acid molecule (or a sequence which is at least 60% identical to the six nucleic acids or their open reading frames, fragments of at least is nucleotides, naturally occurring variants, or a DNA insert of the plasmid deposited with the American Type Culture Collection as Accession No. not defined in the specification, which encodes the amino acid sequence). Also included are a host cell containing the nucleic acids (used to produce the

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                                                                                                                                                                                                                                                                                                                                       New isolated 38650, 28472, 5495, 65507, 81588 and 14354 nucleic acid molecules, useful for diagnosing, treating cancer, pain, or immune, heart, endothelial cell, hematopoeitic, blood vessel, brain, metaboli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-NOV-2000; 2000US-0246768P.
08-NOV-2000; 2000US-0246772P.
15-NOV-2000; 2000US-0249185P.
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                                                                                                                                                                                                                                                                Claim 4; Fig 8; 90pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; enzyme; cancer; aberrant cellular proliferation; differentiation; immune disorders; heart disorder; brain disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human glycoprotease encoded by cDNA 28472.
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Best Local Similarity 9/.~
260; Conservative
                                                                                          Isogai T, Sugryamma
Yamamoto J, Isono Y,
Caki N, Yoshikawa T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic; Gene Therapy; human; secretory protein; membrane proteins; cancer; inflammatory disease; osteoporosis; neurological disease.
                             WPI; 2003-395539/38.
N-PSDB; ADA52832.
                                                                                                                                                                                                                                                                                                                                              14-SEP-2001;
24-JAN-2002;
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2002US-0350435P.
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Pred. No. 4.3e-143;
3; Mismatches 4;
                                                                                                                 T, Wakamatsu A, Sato H, II
Otsuka K, Nagai K, Irie R,
M, Nagahari K, Masuho Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for disease which the gene is involved, or as target molecules for gene therapy.
                                                 Disclosure; SEQ ID NO 34191; 21pp + Sequence Listing; English
                                                                                                                             New isolated nucleic a
genes from Drosophila
                                                                                                                                                                                                             WPI; 2001-656860/75.
N-PSDB; ABL13236.
                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-2000;
11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                       interactions.
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                                                                                                                                                                                                                                                                                         JC,
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2000US-00614150.
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Pred. No. 1.1e-115;
0; Mismatches 3;
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The invention relates

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Best Local Similarity 38.2
Matches 100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating-cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                   Region
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                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana ygjD protein homologue.
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                                               22-APR-1998
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                 (GLAX ) GLAXO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 RRLSLIKHPECSTMSGGKAIEHLAK-QGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKII 117
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                                               9869-00008123.
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208. .259 
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Pred. No. 1.4e-37;
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Matches 100
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 25-FEB-1999;
05-MAR-1999;
                                                                                                                                                            Arabidopsis thaliana.
                                                                                                                                                                                                               Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control;
                                                                                                                                                                                                                                                                                                                                                AAG19287;
                                                                                                                                                                                                                                                                                                                                                                                 AAG19287 standard; protein; 245 AA
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                                                    25-FEB-2000;
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                                                                                                                             EP1033405-A2
                                                                                                                                                                                                    termination
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 MEAHALVARLVEQELSFPFMALLISGGHNILVLAHKLGQYTQLGTTVDDAIGEAFDKTAK
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                                                                                                                                                                                                  sequence.
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 99US-0121825P.
99US-0123180P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.6%; Score 409.5; DB 3; 36.6%; Pred. No. 8.2e-37; tive 37; Mismatches 91;
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promoter;
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<b>ងីងីស៊ីស៊ីស៊ីស៊ីស៊ីស៊ីស៊ីស៊ី</b> ស៊ីស៊ី	אי סי סי סי סי אי אי סי סי א אי סי א א א א	***************************************	PRPRPR
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RESULT 12
AAG19286
ID AAG19286 standard; protein; 439 AA.
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AC AAG19286;
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DT 17-OCT-2000 (first entry)
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                                      Protein identification; signal transduction pathway; metabolic pathway; hybridigation assay; genetic mapping; yene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMK 119
                                                                                                                                                                                                                                                                                                                             HDIEGIRYEPKCP 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                |---:DAKCPVSSATNEDRRNRADIAASFQRVAVLHLEEKCERAIDWALE---LEPSI
                                                                                                           thaliana protein fragment SEQ ID NO: 21030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.8%; Scilarity 38.7%; Pr
Conservative 34;
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99US-0159637P
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99US-0159329P.
                                                                                                                                                                                                                                                                                                           RYDPPPP 231
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Pred. No. 5.6e-3
34; Mismatches
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5.6e-36;
hes 90;
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RESULT 13
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ID AAG19285 standard; protein;
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nilarity 38.7%;
Conservative 3
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99US-0158232P

99US-015929AP

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                                                                             RYDPPPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New Ehrlichia ruminantium polynucleotides, useful as vaccines for inducing protective immunity, and protecting animals or humans against rickettsial diseases, e.g. typhus, spotted fever or heart water.
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LSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKK 120
                                                                                       KYIDN-----DFICNISASFQDCIGDILVNRITNAIHMSQAINCKINK----
                                                                                                                                         EKEEGIEKGQILSSAADIAATVOHTMACHLVKRTHRAI-----LFCKQRDLLPQNNAVLV 175
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Mcguire TC,
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Mahan SM;
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The invention relates to an isolated nucleic acid comprising any one of CC the 6213 antisense sequences given in the specification where expression of the following a promoter operably linked to the nucleic acid comprising a promoter operably linked to the nucleic acid concoding a polypeptide whose expression is inhibited by the antisense concleic acid; (4) a host cell containing the vector; (3) an isolated contisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular composition; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway capable of specifically binding cequired for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation; (8) compound that influences the biological pathway in which a proliferation creditar proliferation or the biological compound is activity; (9) manufacturing an antibotic; (10) profiling a compound's activity; (9) manufacturing an antibotic; (10) profiling a compound's activity; (9) manufacturing an antibotic; (10) profiling a compound's activity; (10) identifying a culture comprising strains in which the gene compound that inhibits proliferation of an organism acts; (10) identifying the target of a compound that inhibits the gene compound is activity; (10) identifying the target of a compound that inhibits the compound compound that inhibits are useful for identifying proteins or accessing for homologous nucleic acids are useful for identifying proteins or for screening bandledens nucleic acids required confidency processes. The solution confidence confidence molecules for rational confidence confidence molecules for rational confidence confidence confidence and confidence confidence confidence.
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 25; SEQ ID NO 50858; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein encoded by Prokaryotic essential gene #8461.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
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discovery programs, or for screening homologous nucleic acids ired for proliferation in cells other than S. aureus, S. typhimurium
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Forsyth RA,
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Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 382 AA;
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                                                                                  GVASNFYIRRALBILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHD
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37.4%; Pred. No. 5.6e-27;
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Sequence 27, Appli Sequence 19, Appli Sequence 19, Appli Sequence 1776, Appli Sequence 1776, Appli Sequence 17372, Appli Sequence 4, Appli Sequence 4, Appli Sequence 28, Appli Sequence 609, Appli Sequence 52, Appli Sequence 52, Appli Sequence 52, Appli Sequence 52, Appli Sequence 52, Appli Sequence 52, Appli Sequence 52, Appli Sequence 52, Appli Sequence 52, Appli Sequence 52, Appli Sequence 52, Appli Sequence 52, Appli Sequence 54, Appli Sequence 54, Appli Sequence 4221, Appli Sequence 4221, Appli Sequence 4956, App Sequence 4956, App Sequence 4956, App Sequence 27, Appli Sequence 278, Appli Sequence 278, Appli Sequence 278, Appli Sequence 213, App Sequence 213, App Sequence 2148, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App Sequence 196, App S
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                                                                                       US-10-067-443-19
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CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                             Sequence 19, Application US/10067443
Patent No. 6642041
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: SOLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR PILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.0
SEQ ID NO 19
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APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYMUCLECTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
                     Matches
                                                   Query Match
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Best Local Similarity
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                                                                                                     LENGTH: 439
TYPE: PRT
ORGANISM: homo
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CURRENT FILING DATE: 2002-02-05
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                                     Local Similarity
                   266;
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                   Mismatches
                                                     DB 4;
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                   Indels
                                                   Length 439;
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US-09-540-236-2726
; Sequence 2726, Application US/09540236
; Patent No. 6673910
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; LENGTH: 463
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-067-443-3
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US-10-067-443-3
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APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REPERENCE: D0073 NP
FILE REPERENCE: D0073 NP
CURRENT PILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR PILING DATE: 2001-02-05
PRIOR PILING DATE: 2001-02-05
PRIOR PILING DATE: 2001-02-05
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PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.0
404
                                               240
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                                                                                                                                        180 VASNFYIRRALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDIEGIRY 239
                                                                                                                                                                                             307
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                                                                                                                                                                                                                                                                                                                                                                                          192 MEAHALVARIVEQELSFPFMALLISGGHNLLVLAHKLGQYTQLGTTVDDAIGEAFDKTAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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DPPPPATEPEDYVYDLRPRWPLGEEYAKGRSEA
                                                                                             VASNKYVRLRLINNI VENKULKLVĆPPPSLČTDNGVMVAWTGLEHPRVG
                                                                                                                                                                                                                                       KEKEEGIEKGQILSSAADIAATVOHTMACHLVKRTHRAILFCKORDLLPONNAVLVASGG 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29.6%; Score 409.5; DB 4; ilarity 36.6%; Pred. No. 8.2e-41; Conservative 37; Mismatches 91;
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                                             PKCPLGVDISKEVGEA
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                                                                                                                                                                                                                                                         ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17372
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US-09-540-236-2726
                                                                                                                                                                     Query Match
Best Local S
Matches 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
FILE REFERENCE: 107196.137
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Best Local S
Matches 84
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CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2726
LENGTH: 350
                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
SEQ ID NO 17372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17372, Ap
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APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARTITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF COMMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
                                                                                                                                                                                                                                                                                                     TYPE: PRT
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                                                                                   172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231 DTPNAQSDP-----ATRADIAASFEYAVVDTLVKKCTKALQMTGIRQ------LVVAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 RRLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIM 118 : : |: | | | | | | | | | | 118
                                     60 ELSLIVUBECSTAGGKAISHLAKQGWKFHFDIKFFLHHAKNCDFSFTGLQHVTDKIIMK 119
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                                                                                                                                                                       87; Conserv
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                                                                                 MEGHLLAPMLEEQPPRFPFVALLVSGGHTQLVRVDGIGRYQLLGESVDDAAGEAFDKTAK 231
                                                                                                                         MEAHALTIRLTNK-VBFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVAR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVASNFYIRRALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAG------ 227
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                                                                                                                                                                   21.0%; Score 291.5; ilarity 35.4%; Pred. No. 1.60 Conservative 37; Mismatches
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-GGPEIARLAERGTPGRFVFPRPMTDRPGLDFSFSGLKTFTLN-TWQ 283
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Pred. No. 1.7e-28;
                                                                                                                                                                   1.6e-26;
ches 99;
                                                                                                                                                                                                          DB 4;
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                                                                                                                                                                                                                                                                      RESULT 8
US-08-087-797-3
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TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT PILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR REPLICATION NUMBER: US 60/128,706
PRIOR PILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 6513
LENGTH: 357
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                                                                                                                                                                                                            GENERAL INFORMATION:
                                      APPLICANT: Mellors, ALG..
APPLICANT: Lo., Reggie Y.C.
APPLICANT: Abdullah, Khalid M.
APPLICANT: Abdullah, Khalid M.
TITLE OF INVENTION: Pasteurella Haemolytica
TITLE OF INVENTION: Glycoprotease
TITLE OF INVENTION: Game and the Furified Enzyme
TITLE OF CROHENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Seltzer, Park & Gibson, P.A.
STREET: 1211 East Morehead Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                238 RYEPKCPL 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 MEGHLLAPMLEEKTPDFPFVALLVSGGHTQLISVTGIGEYTLLGESIDDAAGEAFDKTAK 188
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                                                                                                                                                                                                                                                   Application US/08087797
                                                                                                                                                                                                                                                                                                                                                         TVRPRWPL
                                                                                                                                                                                                                                                                                                                                                                                                                                        GVSANRTLRAKMAMIMEQLGGEVFYARPELCTDNGAMIALAGMIRFKGGTEGPL----GV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GVASNFYIRRALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIBRLRAGL-GILHDIEGI 237
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Pred. No. 3e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3e-25;
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US-10-067-443-4
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                 APPLICANT: Bristol Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR PLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/262,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/10067443
Patent No. 6642041
GENERAL INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,797
FILING DATE: 14-JUL-1993
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
SEQUENCE Amino acids
ACTYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
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Local Similarity 33.6%;
hes 83; Conservative 3
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REFERENCE/DOCKET NUMBER: 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
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; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-067-443-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity
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TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED IN
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR PILING DATE: 2001-04-10
PRIOR PILING DATE: 2001-04-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.0
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les 85; Conservative
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                                                                                                                                            RLRKNSETSID-----IPDFCASLQNTVARHISSKLHIFFESLSEQEKLPKQ---LVI 302
                                                                                                                                                                                           IMKKEKEEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVA 176
                                                                                                                                                                                                                                         QLGDL-GSEFDGIHVGAAVEILASRASADGHLRYPIFLPNVPKANMNFDQIKGSYLNLLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RLSLIKHPECSTMSGGKAIEHLAKQGN---RFHFDIKPPLHHAKNCDFSFTGLQHVTDKI 116
                                                 GGGVAANQYIFGAISKLSAAHNVTTIKVLLSLCTDNAEMIAYSGL---
                                                                                             SGGVASNFY IRRALEIL TNATQCTLLCPPPRLCTDNGIMIAWNG IERLRAGLGILHDIEG
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  IRYEP---
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                                                                                                                                                                                                                                                                                                                                                                                                                               19.9%; Score 276; DB 4; Length 421; 30.4%; Pred. No. 1.4e-24; ative 52; Mismatches 107; Indels
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  -KCPLGVDISKEVGEASIKVPQLKM 265
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                                                                US-09-489-039A-9221
                                                                                   RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPAX: 704 33% 20 TIMPORMATION FOR SEQ ID NO: 2 SEQUENCE CHARACTERISTICS: LENGTH: 325 amino acids TYPE: amino acids TYPE: amino acids TYPE: inear
                      Sequence 9221, Application Patent No. 6610836
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08087797 Patent No. 5543312
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Seltzer, Park & Gibson,
ADDRESSEE: Park Morehead Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: LAYTON, Jr., Samuel G.
REGISTRATION NUMBER: 22807
REFERENCE/DOCKET NUMBER: 337-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,797
FILING DATE: 14-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Abdullah
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Mellors, Alan
APPLICANT: Lo, Reggie Y.C.
APPLICANT: Abdullah, Khalid M.
TITLE OF INVENTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 141.
STREET: 161.
CITY: Charlotte
CTATE: No. 5543312th Carolina
""ited States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 70% 334 2014
                                                                                                                                               274 VSANKQLRADLAEMMKKLKGEVFYPRPQFCTDNGAMIAYTGFLRLK 319
                                                                                                                                                                                         180 VASNFYIRRALBILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLR 225
                                                                                                                                                                                                                                                                                                                                                                                                           112 MEGHLLAPMLEENAPEFPFVALLISGGHTQLVKVDGVGQYELLGESIDDAAGEAFDKTGK 171
                                                                                                                                                                                                                                                                                                                                                               60 RLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MEAHALTIRL-TNKVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVAR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79;
                                                                                                                                                                                                                                   NLNENGELDEQ---TKCDIAHAFQQAV-----VDTILIKCK-RALEQTGYKRLVMAGG
                                                                                                                                                                                                                                                                             KEKEEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGG 179
                                                                                                                                                                                                                                                                                                                       LLGL-DYP-----AGVAMSKLAESGTPNRFKFPRPMTDRPGLDFSFSGLKTFAANTIKA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  325 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.5%; Score 270.5; DB 1; Length 325; 35.0%; Pred. No. 4.2e-24; ative 26; Mismatches 102; Indels 19;
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Glycoprotease
Gene and the Purified Enzyme
                                         US/09489039A
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RESULT 13
US-09-107-532A-6609
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                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 9221
LENGTH: 343
TYPE: PRT
ORGANISM: Klobsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gary Breton et. al TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                    APPLICATION NUMBER: US/09/107,532A FILING DATE: 30-Jun-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                             ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/RC
                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 RYEPKCPL 245
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                                                                         APPLICATION NUMBER: 60/085,598 FILING DATE: 14 May 1998 APPLICATION NUMBER: 60/051571 FILING DATE: July 2, 1997
                                                                                                                                                                                                                                  COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TVRPRWPL 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NGDDE-----QTRADIARAFEDAVVDTLMIKCRRA-----LEQTGFKRLVMAG
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                NAME: Ariniello, Pamela Deneke REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                          STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                             CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 100 Beaver Street
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSES: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.4%; Score 268.5; DB 4; 32.7%; Pred. No. 8.1e-24; tive 31; Mismatches 105;
                                                                                                                                                                                                                                                                                               CD/ROM ISO9660
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TELECOMMUNICATION INFORMATION:

(781)893-5007

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US-08-987-121A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                     TELEPHONE: 317-276-3334 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (781)893-501
TELEPAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6609:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hoskins, or many APPLICANT: Tang, Joseph Chiou-Chung APPLICANT: Treadway, Patti Jean APPLICANT: Treadway, Patti Jean or INVENTION: Streptococcus Pneumoniae Gene Sequence
                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                         REFERENCE/DOCKET NUMBER: X-
TELECOMMUNICATION INFORMATION:
                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,872
                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSE: Eli Lilly and Company
STREET: Lilly Corporate Center
  SEQUENCE
                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...363
SEQUENCE DESCRIPTION: SEQ ID NO: 6609:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200 LGL----SYPSGKEIDQLAHQGKDNYHF--PRAMIHEDNYDFSFSGLKSAFINLVHN 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LSLIKHPECSTMSGGKAIEHLAKQG-NRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMK 119
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                                                                                                                                                                                                                                                                                                                                                                   46285
                                                                                                                                                                                                                                                                                                                                                                                                                             Indianapolis
CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGGVASNFYIRRALEILTNA--TQCTLLCPPPRLCTDNGIMI 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/08987121A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGVAANQGLREGLQAALSAKLPEVELVIPPLRLCGDNAAMI 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQQRGEDLDKN---
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TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                           Indiana
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                                                                                                                                                                                                            US/08/987,121A
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                                                                                                                                                                                                                                                      Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78;
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-987-121A-4
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                                                                               US-08-961-083-52
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Query Match 18.:
Best Local Similarity 32.0
Matches 72; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 18.3%; Score 254; DB 3; Best Local Similarity 32.4%; Pred. No. 4.6e-22; Matches 73; Conservative 36; Mismatches 86
                                                                                                                                                                                            TELEFAX: (301) 309-851
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: HP Vectra 486/
OPERATING SYSTEM: MSDOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/(
                                                                                                                                                                                                                                                                     NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB:
TELECOMMUNICATION INFORMATION:
                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Choi et.
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                  TOPOLOGY: linear
                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Rockville
                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 MAGHLMAAQSVEPLEFPLLALLVSGGHTELVYVSEAGDYKIVGETRDDAVGEAYDKVGRV 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 ASNFYIRRALEILTNATQCTLLCPPPRLCTDNGIMIA-----WN 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 LSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKK 120
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                                                                                                                                                                        335 amino acids
                                                                                                                                                                                                                                     (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Genome Sciences,
                                                                                                                                                                                                                                                       (301)
                                                                                                 protein
                     18.1%; Score 250; DB 3; 32.0%; Pred. No. 1.4e-21;
                                                                                                                                                                                                                                                       309-8504
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                                       Length 335;
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36;

Mismatches

Indels

30;

Gaps

. 70	1 MEAHALTIRLTNKVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARR 60	
Db	114 MAGHLMAAQSVEPLEFPLLALLVSGGHTELVYVSEAGDYKIVGETRDDAVGEAYDKVGRV 173	
ş	61 LSLIKHPECSTMSGGKAIEHLAKQGNREHEDIKPPLHHAKNCDFSETGLQHVTDKIIMKK 120	
DЬ	174 MGLTYPAGREIDELAHQGQDI-YDFPRAMIKEDNLEFSFSGLKSAFINLHHNA 225	
δ.	121 EKEEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGV 180	
₽	226 EQKGESLST-EDLCASFQAAVMDILMAKTKKALEKYPVKILVVAGGV 271	
Ş	181 ASNEYIRRALEILTNATQCTLLCPPPRLCTDNGIMIAWN 219	
₽	272 AANKGLRERLAAEITDVKVIIPPLRLCGDNAGMIAYASVSXWN 314	
search o	Search completed: February 16, 2005, 13:10:25	

Search completed: February 16, 2005, 13:10:25 Job time : 16.962 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                               1385
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l: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
                                                                                                                                                                                                                                                                                           Length
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                                                                                                                                                                                                                                                                                               В
US-10-067-443-22

US-10-649-273-22

US-10-651-722-22

US-10-649-273-2

US-10-649-273-2

US-10-661-722-2

US-10-649-273-19

US-10-649-273-19

US-10-649-273-19

US-10-651-722-19

US-10-651-722-19

US-10-651-722-19

US-10-094-749-2039

US-10-094-749-2039

US-10-0424-599-209259
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## ALIGNMENTS

RESULT 1 US-10-067-443-22

Application US/10067443

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SEQ ID NO 22
LENGTH: 267
TYPE: PRT
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22, Application US/100 Publication No. US20030082782A1 GENERAL INFORMATION:
                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 267; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED IN
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/282,814
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2001-04-10 NUMBER OF SEQ ID NOS: 71
  121 EKBEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLFQNNAVLVASGGV 180
                                              61
                                                                  51 LSLIKHTSCSTWGGGKÄIEHLÄKKGGKRFRFDIKFFLHHÄKKÜDFSFTGLGHVTDKIIMKK 120
                                                                                                                                                 1 MEAHALTIRLTNKVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARR 60
                                                                                                                                                                                                                 h 100.0%; Score 1385; DB 14; Length 267;
Similarity 100.0%; Pred. No. 1.8e-139;
67; Conservative 0; Mismatches 0; Indels 0;
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CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
Sequence 22, Application US/10651722

Publication No. US20040048302A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE, MP-1

FILE REFERENCE: DO073 DIV

CURRENT APPLICATION NUMBER: US/10/651,722

CURRENT PILING DATE: 2003-08-29

PRIOR APPLICATION NUMBER: US 60/266,518

PRIOR PILING DATE: 2001-02-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.2
SEQ ID NO 22
LENGTH: 267
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Publication No. US20040043407A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE,
FILE REFERENCE: D0073 CNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tch 100.0%; Score 1385; DB 15; al Similarity 100.0%; Pred. No. 1.8e-139; 267; Conservative 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 414
TYPE: PRT
ORGANISM: Homo sapiens
US-10-067-443-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/10067443
Publication No. US20030082782A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
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PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.2
SEQ ID NO 22
TAXABLE: PATENTIN OF SEQ ID NO 22
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Best Local
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                                                                                                                  Similarity
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                                        LSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKK 267
                                                              LSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKK 120
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Sequence 2, Application US/10651722

Publication No. US20040048302A1

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIOE ENCODING A 1
FILE REFERENCE: D0073 DIV
GURRENT APPLICATION NUMBER: US/10/651,722
CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
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CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PATENTIN NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PATENTIN NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PATENTIN NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
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Publication No. US20040043407A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE,

FILE REFERENCE: D0073 CNT
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; PRIOR APPLICATION NUMBER: US 10/067,443;
PRIOR FILING DATE: 2002-02-05;
PRIOR APPLICATION NUMBER: US 60/282,814;
PRIOR FILING DATE: 2001-04-10;
NUMBER OF SEQ ID NOS: 71;
SOFTWARE: PatentIn version 3.2;
SEQ ID NO 2;
LENGTH: 414;
TYPE: PRT
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Publication No. US20030082782A1
GENERAL INFORMATION:
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Best Local :
                                                                                                                                                                                                                                                                                                                        Matches 266; Conservative
                                                                                                                                                                                                                                                                                                                                                  Query Match 98.1%;
Best Local Similarity 91.1%;
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TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
CONTRADED: DESCRIPTION SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF SECONDARY OF S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 439
TYPE: PRT
ORGANISM: homo sapiens
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ORGANISM: Homo sapiens
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                                                                                                                                                                                         EKBEGI ---
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                                                                                                                                                                                                                                                                                                                  Score 1358.5; DB 14
Pred. No. 2.5e-136;
0; Mismatches 1;
      ----EKGQILSSAADIAATVQHTMACHLVKRTH 155
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US-10-651-722-19
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Sequence 19, Application US/10651722

Publication No. US20040048302A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1

FILE REFERENCE: D0073 DIV

CURRENT EPLICATION NUMBER: US/10/651,722

CURRENT FILING DATE: 2003-08-29

PRIOR APPLICATION NUMBER: US 60/266,518

PRIOR FILING DATE: 2001-02-05
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PRIOR PILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.2
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19, Application US/106 Publication No. US20040043407A1 GENERAL INFORMATION:
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CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
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TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE,
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ORGANISM: homo sapiens
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|KEEGIFLISKVEQINIPGLCLKIAAHFCRYEKGQILSSAADIAATVQHTMACHLVKRTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSL1KHPECSTMSGGKA1EHLAKQGNRFHFD1KPPLHHAKNCDFSFTGLQHVTDK1IMKK
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PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.2
SEQ ID NO 19
LENGTH: 439
TYPE: PRT
ORGANISM: homo sapiens
US-10-651-722-19
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                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo
US-10-012-140-5
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US-10-012-140-5
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                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/012,140
CURRENT FILING DATE: 2001-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR PELICATION NUMBER: 60/246,768
PRIOR APPLICATION NUMBER: 60/246,772
PRIOR FILING DATE: 2000-11-08
PRIOR PELICATION NUMBER: 60/249,185
PRIOR FILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                         Matches
                                                                                        Query Match
Best Local
                                                                                                                                                                                                                      SEQ ID NO 5
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: 38650, 28472, 5
TITLE OF INVENTION: 14354 METHODS
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 381552004900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 10/067,443 PRIOR FILING DATE: 2002-02-05
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                                                                                                                                                                                                     ENGTH: 414
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Local Similarity 91.1%;
                                                                                      Local Similarity
148
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                                                                         260;
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MEAHALTIRLTNKVBFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARR
                   MEAHALTIRLTNKVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARR 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glucksmann, Maria
                                                                         Conservative
                                                                                                                                                                    sapiens
                                                                                        97.3%;
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                                                                       Score 1348; DB 14;
Pred. No. 3.1e-135;
3; Mismatches 4;
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les 1;
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 207
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APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 08435/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILLING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILLING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2039
LENGTH: 364
TYPE: PRT
ORGANISM: Homo sapiens
US-10-094-749-2039
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US-10-094-749-2039
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                                                                                                                                                                                                                       Matches 214; Conservative
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Local Similarity 98.6%;
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                              EKEEGIEKGQILSSAADIAATVQHTWACHLVKRTHRAILFCKQRDLLFQNNAVLVASGGV 180
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OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
ASNFYIRRALBILTNATQCTLLCPPPRLCTDNGIMIA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTSUKA, KAORU
NAGAI, KEIICHI
IRIE, RYOTARO
TAMECHIKA, ICHIRO
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YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
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                                                                                                                                                                                                                                    Score 1105; DB 15; Pred. No. 2.6e-109;
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                                                                                                                                                                                                                                                    Length 364;
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                                              SEQ ID NO 3
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              LENGTH: 463
TYPE: PRT
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_3098C.1.pep US-10-424-599-209259
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Publication No. US20030082782A1
GENERAL INFORMATION:
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APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 209259
                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR PILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR PILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
PILE REFERENCE: D0073 NP
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                                                                                                                             SOFTWARE: PatentIn version 3.0
ORGANISM: Arabidopsis thaliana
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ORGANISM: Glycine max
FEATURE:
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Local Similarity 41.6%; Pred. No. 4.1e-36;
hes 104; Conservative 32; Mismatches 89; Indels 25;
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CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
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Publication No. US20040043407A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.2 SEQ ID NO 3
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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                                                                                                                                                                                                                                              252 WIGLDWH-----RSGGPAVEBLALEGDAKSVKPNVPMKYHKDCNFSYAGLKTQVRLAIEA 306
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                                                                   VASNKYVRLRLNNI VENKNI KLVCPPPSLCTDNGVMVAWTGLEHFRVG--
                                                                                                          VASNFYIRRALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDIEGIRY 239
                                                                                                                                                                                                  KEKEEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGG 179
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                                                                                                                                                          KE-----IRNRADIAASFORVAVLHLEEKCERAIDWALE---LEPSIKHMVISGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  29.6%; Score 409.5; DB 15; Length 463; 36.6%; Pred. No. 1.1e-34;
PKCPLGVDISKBVGEA 256
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LENGTH: 463;
; TYPE: PRT;
; ORGANISM: Arabidopsis thaliana
US-10-651-722-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: D0073 DIV
CURRENT APPLICATION NUMBER: US/10/651,722
CURRENT FILING DATE: 2003-08-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y Match 29.6%; Score 409.5; DB 15; Length Local Similarity 36.6%; Pred. No. 1.1e-34; hes 100; Conservative 37; Mismatches 91; Indels
404 DPPPPATEPEDYVYDLRPRWPLGEEYAKGRSEA 436
                                                                                                                          180 VASNFYIRRALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDIEGIRY 239
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                                                                                                                                                                                                   -- IRNRADIAASFORVAVLHLEEKCERAIDWALE---LEPSIKHMVISGG 353
                                              --PKCPLGVDISKEVGEA 256
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Search completed: February 16, 2005, 13:28:30 Job time: 155.686 secs

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Result
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-MODEL-frame+ p2n.model -DEV=Xlh
-Q-/Ggn2 1/USPTO_Spool/US10649273/runat 14022005_114702_16399/app_query.fasta_1.1429
-DB=GenEmb1 -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXX=0
-UNITS-bits -START=1 -EXD=-1 -MARTX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCOME=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=50 -MINLEN=0 -MAXLEN=200000000
-USER-US10649273_@CGN 1 1 8655_@runat_14022005_114702_16399 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MARIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPDF=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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## ALIGNMENTS

Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match:	TITLE JOURNAL FEATURES SOUTCE	SOURCE ORGANISM REFERENCE AUTHORS	AR541929 LOCUS DEFINITION ACCESSION VERSION
cores: llarity: Similarity:	Zhang, J Zi Wang, D. and Wang, D. acid Nucleic acid Patent: US ( Loo Loo /mc	Unknown. Unknown. Unclassified. 1 (bases 1 to 1416) Tang, Y.T., Zhou, P.,	AR541929 Sequence 177 from paten AR541929 AR541929.1 GI:53934009
1.376-126 1385.00 100.00% 100.00%	Zhang, J., Zhao, Q.A., Yang, Y., Xue, A.J Wang, D. and Drmanac, R.T. Nucleic acids and polypeptides Patent: US 6743619-A 177 01-JUN-2004; Location/Qualifiers 11416 11416 /mol_type="genomic DNA"	to 1416) thou, P., Goods	it i
Leigin: Matches: Conservative: Mismatches: Indels:	<pre>Zhang,J., Zhao,Q.A., Yang,Y., Xue,A.J., Wehrman,T., Wang,JR., Wang,D. and Drmanac,R.T. Nucleic acids and polypeptides Nucleic acids and polypeptides Patent: US 6743619-A 177 01-JUN-2004; Location/Qualifiers 11416 . /organism="unknown" /mol_type="genomic DNA"</pre>	Unknown. Unknown. Unclassified. 1 (bases 1 to 1416) Tang, Y.T., Zhou, P., Goodrich, R., Liu, C., Asundi, V., Ren, F.,	1416 bp DNA US 6743619.
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	wang,JR.,	Ren, F.,	PAT 08-OCT-2004

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Unclassified.

1 (bases 1 to 1526)

1 (bases 1 to 1526)

Chen, J., Feder, J.N., Nelson, T.C., Krystek, S.R. and Duclos, F. Polynucleotides encoding a novel metalloprotease, MP-1
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                                                                              CysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyVal
                                                                                                                                                                                                                       ThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeuPhe
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                    ProGlnLeuLysMetGluIle
                                                       ProLysCysProLeuGlyValAspIleSerLysGluValGlyGluAlaSerIleLysVal
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                                             CCAMATGTCCTCTTGGAGTAGACATATCAAAAGAAGTTGGAGAAGCTTCCATAAAAGTA
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Location/Qualifiers
1. .1526
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REFERENCE
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu.X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                        CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Akhter, N. Ayele, K. Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Districh, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, B., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A. Zhang, I., H. and Green, R.D.
                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 28 Row: i Column: 22.
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
On Dec 19, 2003 this sequence version replaced gi:15080281.
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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1 (bases 1 to 1908)
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Clone MGC:20293 IMAGE:4121450), complete cds.
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CysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyVal 180
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Sequence 1 from I
AR428803
AR428803.1 GI:40
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Chen, J., Feder, J.N., Nelson, T.C., Krystek, S.R. and Polynucleotides encoding a novel metalloprotease, M Patent: US 6642041-A 1 04-NOV-2003;
Location/Qualifiers
1. .2197
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                                                                                                              LeuSerLeuI1eLysHisProGluCysSerThrMetSerGlyGlyLysAlaI1eGluHis
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                                                                                                  CTTTCTTTAATAAAACATCCAGAGTGCTCCACCATGAGTGGTGGGGAAAGCCATAGAACAT
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                                                                                                                                                                                                                                                                        Unclassified.
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1 (bases 1 to 1387)
1 (bases 1 to 1387)
1 (chen, J., Feder, J.N., Nelson, T.C., Krystek, S.R. and Duclos, F. Chen, J., Feder, J.N., Nelson, T.C., Krystek, S.R. and Duclos, F. Chen, J., Feder, J., Nelson, T.C., Krystek, S.R. and Duclos, F. Chen, J., Nelson, T.C., Krystek, S.R. and Duclos, F. Chen, J. Nelson, T.C., Krystek, S.R. and Duclos, F. Chen, J. Nelson, T.C., Krystek, S.R. and Duclos, F. Chen, J., S.R., Localities and J. 1387
Location/Qualifiers
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Sequence 21
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                                                                                                  MetGluAlaHisAlaLeuThrIleArgLeuThrAsnLysValGluPheProPheLeuVal
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                                                                                                                                              Homo sapiens mRNA for putative sialog AJ295148.1 GI:11071726 metallopeptidase; sialoglycoprotease. Homo sapiens (human)
                                                                 Cloning and sequencing of a second human sialoglycoprotease homologue Unpublished
                                                2 (bases 1 to 1387)
Chen, J.M.
                  Submitted (27-CCT-Züüü) Chen J.M., MRC Molecular Enzymology
Laboratory, The Babraham Institute, Babraham, Cambridge, CB2 4AT,
                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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US-10-649-273-2\_COPY\_148\_414 (1-267) x HSA295148 (1-1387) MetGluAlaHisAlaLeuThrIleArgLeuThrAsnLysValGluPheProPheLeuVal ArgAlaIleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuVal AlaAspIleAlaAlaThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHis 155 GluLysGluGluGlyIle-----ASTCYSASDPheSerPheThrGlyLeuGlnHisValThrASDLYSIleIleMetLYSLYS LeuAlaLysGlnGlyAsnArgPheHisPheAspIleLysProProLeuHisHisAlaLys LeuLeuIleSerGlyGlyHisCysLeuLeuAlaLeuValGlnGlyValSerAspPheLeu CTTTCTTTAATAAAACATCCAGAGTGCTCCACCATGAGTGGTGGGAAAGCCATAGAGCAT LeuSerLeuI1eLysHisProGluCysSerThrMetSerGlyGlyLysAlaI1eGluHis CTTCTTGGAAAGTCTTTGGACATAGCACCAGGTGACATGCTTGACAAGGTGGCAAGAAGA LeuLeuGlyLysSerLeuAspIleAlaProGlyAspMetLeuAspLysValAlaArgArg CTTTTGATTTCTGGAGGTCACTGTCTGTTGGCATTAGTTCAAGGAGTTTCAGATTTTCTG TGCCTAAAAATAGCTGCTCATTTCTGCAGGTATGAGAAGGGGGAAATCCTGTCTTCAGCA GAAAAAGAGGAAGGTATATTTCTAATTAGTAAAGTTGAACAGATAAATATTCCTGGATTG 175 1004 1064 135 884 100 944 120 644 824 764 704 80 584 40 524 20 126 60

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Sequence 6 from Patent WO02074960.
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Sequence 4 1
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                                                                                                                                                                                                                                                                                                                                                                                                 Millennium Pharmaceuticals, Inc.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                            of human proteins and uses thereof Patent: WO 02074960-A 4 26-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leiby,K.R., Kapeller-Libermann,R. and Glucksmann,M. 38650, 28472, 5495, 65507, 81588 and 14354 methods
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VEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECST
MSGGKALBHLAKQGNR PHPLIKPLLHAKNCDPS-FGLOHVTDKVARRKQEBGIEKG
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/protein_id="CAD80044.1"
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AUTHORS
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JOURNAL
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MEDLINE
                                                                                                                                                                                                                                      source
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Klausner, R.D., Collins, F.S., Wagner, L., Schaefer, C.F., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buctow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heich, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Willalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Boutfard, G.G., Blakesley, R. W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
DAR 2018R57
                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 123 Row: d Column: 22
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21312463.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web Rire. here: (NISC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (15-SEP-2003) National Institutes of Health, Mammalian Submitted (15-SEP-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Alege,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karline,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,B.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tissue Procurement: Gilbert Smith, Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.B. Consortiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NISA

NIH-MGC Project URL: http://mgc.nci.nih.

Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg, R.
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
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/tippuc_type-"Mammary Lumor metastatized to lung. To arose spontaneously from a senescent normal mammary (clonal) outgrowth infected with the virus MMTV." /clone_lib="NCI CGAP_Lu29" /lab_host="DH10B"
                                                                                             /clone="MGC:67870 IMAGE:5012054"
/tipouc_type-"Mammary Lumor metas
                                                                                                                                             /db_xref="taxon:10090"
                                                                                                                                                                /strain="CZECH II"
                                                                                                                                                                                                              organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mouse!
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Sciurognathi; Muridae;
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US-10-649-273-2_COPY_148_414 (1-267)
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Best Local Similarity:
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LeuLeuCysFroProArgLeuCysThrAspAsnGlyIleMetIleAlaTrpAsnGly 220
                                                                                                     AlaSerAsnPheTyrIleArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThr 200
                                                                                                                                                                                                                                                                                      ThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeuPhe 160
                                                                                                                                                                                                                                                                                                                                                                           GluLysGluGluGlyIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAla 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AsnCysAspPheSerPheThrGlyLeuGlnHisValThrAspLysIleIleMetLysLys 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuAlaLysGlnGlyAsnArgPheHisPheAspIleLysProProLeuHisHisAlaLys 100
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                                                                                                                                                                                                    CysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyVal 180
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                                                                                                                                                                  TGCAAGCAGAAAAATTTGCTATCTCCAGCTAACGCAGTATTAGTTGTATCTGGAGGTGTT
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possible chaperone activity [Posttranslational
modification, protein turnover, chaperones]"
/db_xref="CDD:COG0533"
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QILSSAADIAAAVQHATACHLAKRTHKAILFCKQKNLLSPANAVLVVSGGVASNLYIR
KALEIVANATQCTLLCPPPRLCTDNGIMIAMNGIERLKAGLGVLHDVEDIRYEPKCPL
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RITPSDLSAIATTIKPGLALSLGVGLSFSLQLVNRFKKPFIPIHHMBAHALTIRLTNK
VEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECST
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/protein id="AAH58172.1"
/db xref="G1:34849664"
/translation="MLMLRRTAGAIPKPPKSKVYGFLRRFSVHPRTLSCHKLVLGIET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pCMV-SPORT6"
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1231.00
92.88%
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Matches:
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Villalon, D.K., Muzny, D.M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, J., Smallus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and mouse cDNA sequences
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Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hisiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvanah Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (25-OCT-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                  Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Genome Sequence Centre,
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903
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                                                                                                                                                                                                                                       BC Cancer Agency, Vancouver, BC, Canada
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                             CysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyVal 180
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 IleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAspIleGluGlyIleArgTyrGlu
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/clone="IMAGE:5053599"
/tissue_type="Liver, normal. 5 month old male mouse.
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Helix Research Institute (JP) ; Resea
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Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Obayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Obayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Obayashi, K., Yasuda, T., Tanaka, T., Tanaka, T., Tanaka, T., Shibahari, K., Yamamoto, J., Sato, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Marakami, K., Yasuda, T., Iwayanagi, T., Wagateuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Siyawara, M., Takahashi, M., Kanda, K., Yokoi, T., Puruya, T., Kikawa, B., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tarihami, K., Takahashi, T., Yamashita, H., Minaka, S., Ono, Y., Takiguchi, S., Watanabe, M., Hiraoka, S., Yohika, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosikawa, Y., Matsunawa, H., Ichihara, T., Sasaki, N., Actsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Sasaki, N., Actsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Sasaki, N., Sazo, S., Moriya, S., Moniyana, H., Satoh, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyana, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Tich, T., Shigeta, K., Senba, T., Yamada, K., Fujii, Y., Ozaki, K., Tich, T., Shigeta, K., Senba, T., Kawakami, T., Kobatake, N., Nakajama, M., Hata, H., Watanabe, M., Watanabe, T., Nakajawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakajawa, K., Okamara, K., Nakagawa, K., Okamura, 
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2208 bp mRNA linear PRI 30-JAN-2004
sapiens cDNA FLJ30879 fis, clone FEBRA2004592, highly similar
como sapiens mRNA for putative sialoglycoprotease type 2.
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Primates;
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Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M.,
Kimura,K., Yamashita,H., Matsuo,K., Murakawa,K., Kanchori,K.,
Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanchori,K.,
Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y.,
Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
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Isogai,T., Otsuki,T. and Sugiyama,T.
Direct Submission
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LeuLeuGlyLysSerLeuAspIleAlaProGlyAspMetLeuAspLysValAlaArgArg
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GVSBSDLSAIATIKEGIALSLGVGLSFSLQLVGQLKKPFIPHMBAHALTIRLTNK
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MSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFPFTGLQHVTDKIIMKKEKEBGIEKG
QILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNFCIR
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/clone_lib="FEBRA2"
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Matches:
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Indels:
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VERSION
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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
Strausberg, R.L., Peingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.P., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.R., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.M.,
Villalon, E.K., Wunzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,
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BC078974
                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Norway rat)
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                                                                                                                                                                                                                                                                                                                                                                                                           Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAAAAGAGGAAGGTATTGAGAAGGGGCAAATCCTGTCTTCAGCAGCAGACATTGCTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProLysCysProLeuGlyValAspIleSerLysGluValGlyGluAlaSerIleLysVal 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAspIleGluGlyIleArgTyrGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuLeuCysProProProArgLeuCysThrAspAsnGlyIleMetIleAlaTrpAsnGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCAAGTAACTTCTGTATCCGCAGAGCTCTGGAAATTTTAACAAACGCAACACAGTGCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GluLysGluGluGlyIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAla 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --- TGATGTCCTCTTGGAGTAGACATATCAAAAGAAGTTGGAGAAGCTTCCATAAAAGTA 1492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTAAGCAGAGAGACTTGTTACCTCAAAATAATGCAGTACTGGTTGCATCTGGTGGTGTC
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IMAGE:7111906,
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Percent Similarity:
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COMMENT
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AUTHORS
                                          8
                                                                                             US-10-649-273-2_COPY_148_414 (1-267)
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                                                                                                                                                                                                                                                            Score:
                                                                                                                                                                                                                                                                                    Pred. No.:
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PUBMED
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Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LIMI at: http://image.llnl.gov Series: IRAK Plate: 182 Row: f Column: 6
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (02-AUG-2004) National Institutes of Health, Mammalian Submitted (02-AUG-2004) Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: Express Genomics CDNA Library Arrayed by: The I.M.A.G.E. COMSORTIUM (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Howard Jacobs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 1546)
Director MGC Project.
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Proc. Natl. Acad. Sci. U.S.A. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site:
                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/product="Unknown (protein for IMAGE:7111906)"
/protein id="AAH78974.1"
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VGFPFLVLLISGGHCLLALVQSVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECST
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QILSSAADIAAAVQHATACHLAKRTHRAILFCQQKULLSPANAVLVVSGGVASNLYIR
RALEIVANATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGIGIIHDVEDIRYEPKAGE
INSMLTJALTEDLDSVSSTHTVAHSPLNSGSRGANIQTSMCSCTQTVYMRTVRHTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Testis, rat
/clone_lib="NIH_MGC_237"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="Vector: pExpress1"
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                                                                                                                                                                                                                                                         Length:
Matches:
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USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Marcello Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, University of CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
NNA Seguencing by: Institute for Systems Biology
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Mus musculus, clone IMAGE:1327545,
BC051211
BC051211.1 GI:29881634
                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
1 (bases 1 to 1109)
Strausberg,R.
                                                                                                                                                     Submitted (14-APR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
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This clone was selected for full length sequencing because it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Brin Helton, Mark Ketteman, Anura
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       analysis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.systemsbiology.org
                              ValAlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCys
                                                                                                                                                            AlaThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeu 159
                                                                                                                                                                                                                  LysGluLysGluGluGlyIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIleAla
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                                                                                             PheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGly
                                                                                                                                        GCTGCGGTACAGCATGCAACAGCGTGCCACCTTGCGAAAAGAACACATCGCGCTATTCTG
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/clone lib="Soares_thymus_2NbMT"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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/clone="IMAGE:1327545"
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Gallus gallus
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST cDNA collection, from a library constructed by Blizabeth Bosch. cDNA was prepared from RNA extracted from muscle, normalised, and poly A-trimmed. EcoRI-NotI cut cDNA was then ligated into the vector. Vector: political intervals in the vector of the vector of the vector of the vector of the vector.
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (02-FEB-2004) Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: chickest@bms.umist.ac.uk
BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequencing project.
This sequence is from the
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                                MetGluAlaHisAlaLeuThrIleArgLeuThrAsnLysValGluPheProPheLeuVal
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LeuLeuIleSerGlyGlyHisCysLeuLeuAlaLeuValGlnGlyValSerAspPheLeu 40
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/dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                                 /strain="Layer and broiler"
/db_xref="taxon:9031"
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Search completed: February 16, 2005, 18:02:51 Job time : 4263.78 secs

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-MODEL-frame+_p2n.model -DEV=x1h
-Q=/cgn2_1/USPTO_spool/US1649273/runat_14022005_114702_16389/app_query.fasta_1.1429
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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Human; gene; ss; nervous system disorder; peripheral neuropathy; Huntington's disease; amyotrophic lateral sclerosis; haemophilia; neurodegenerative disease; Parkinson's disease; Alzheimer's disease	75.			ס מיי.		ALIGNMENTS	ACA51431	AAS56045	ACA44384 ADF02056	ADT05644	ADT05493	MAI42063_05		AAS53309	ADG73343	ABD02280	ADG73341	ACA42146	ABQ90383	ABK37804	AAF91424	ADL03120 ACA43173	AAF28551	ACA39102	ACA26804 ACA20445	AAH15110	AAD48239	AAC38454	ABL24633 ABL24632	ADL86726	ADL86725	AAS84622	ARO75508	ADQ24627	ADA52832	ABS57020	AAD46856 ACA60887
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neurodegenerative disease; rarkinson's disease; alleamet subtense; autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis; insulin-dependent diabetes mellitus; anaemia; thrombocytopaenia; wound; ulcer; burn; bone disorder; osteoporosis; osteoarthritis; stroke; fibrosis; reperfusion injury; infection; allergic rhinitis; asthma; coagulation disorder; cancer; tumour; inflammatory disease; septic shock; Homo haemostatic; Crohn's disease; anaphylaxis; proliferation; chemotactic; differentiation; stem cell growth factor; haematopoiesis; chemokinetic; sapiens. antiinflammatory; expressed sequence tag; EST.

Result No.

Score

Query Match

Length

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Description

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

WO200281731-M2

29-JAN-2002; 2002WO-US001222.

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CC Alzheimer's disease); autolimnume disease (e.g. systemic lugus (erythematosus, rheumatoid arthritis, insulin-dependent diabetes mellitus); myeloid or lymphoid cell disorders (e.g. anaemia and thrombocytopaemia) (c); wounds, ulcers, burns; bone disorders (e.g. osteoporosis, osteoarthritis); mechanical and traumatic disorders (e.g. stroke, head (trauma); lung or liver fibrosis; reperfusion injury in various tissues; bacterial, viral or fungal infections; allergic conditions such as coagulation disorders (e.g. haemophilia); (c) cancer and tumours; and inflammatory diseases (e.g. haemophilia); (c) disease, anaphylaxis). The protein may be used to inhibit the growth, (c) infection or function of infectious agents such as bacteria, fungi, (c) viruses, or to effect bodily characteristics, biorhythms or circadian (c) cycles of rhythms. The protein may also have (c) proliferation/differentiation, stem cell growth factor, haematopoiesis (e) cregulation, immune stimulating or suppressing, chemotactic/chemokinetic, haemostatic and thrombolytic, receptor/ligand, and antiinflammatory cactivities. The cDNA sequences of the invention are useful for expressing recombinant protein for analysis. The present sequence represents a novel human cDNA sequence of the invention, this sequence is an expressed sequence tag (EST) and was identified using subtractive hybridisation
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Best Local Similarity:
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                                                                                                                                                                                                                                                                               Claim 5; Page 29-30 (Disclosure); 38pp; Chinese.
                                                                                                                                                                                                                                                                                                                              O-sialogycoproteinase-like protein and encoding polynucleotide, useful for diagnosing, preventing and treating related diseases.
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The present sequence encodes human O-sialoglycoproteinase-like protein (OSGPLP). The present invention also describes: (1) the preparation of the OSGPLP protein; (2) applying the OSGPLP protein in diagnosis; (3) the prevention and/or treatment of related diseases; (4) utilising the OSGPLP protein in screening its agonist, excitomotor and inhibitor and preparing an antibody against the CSCPLP protein, aid (3) the use of the USGPLP polynucleotide sequences, proteins, agonists, excitomotors, inhibitors and antibodies in treating diseases related to the abnormal OSGPLP gene and in preparing the medicine composite for the treatment

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Best Local Similarity:
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Metalloprotease; MP-1; immune disorder; glutamate transport; cancer; motor neuron disorder; amyotrophic lateral sclerosis; ALS; diabetes; reproductive disorder; Kleinfelter's syndrome; germinal cell aplasia; genital wart; metabolic disorder; premature puberty; Kallman syndrome; Cushing's syndrome; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; Huntington's disease; Tourette syndrome; sepsis; liver disease; renal disease; fimmune disorder; rheumatoid arthritis; acquired immunodeficiency syndrome; AIDS; pulmonary disease; pneumonia; emphysema; cystic fibrosis; vascular disorder; inflammatory disorder;
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05-FEB-2001; 2001US-0266518P. 10-APR-2001; 2001US-0282814P. 05-FEB-2002; 2002WO-US003353 (BRIM ) BRISTOL-MYERS SQUIBB Ç Feder J, Nelson TC, 8 Έ, Krystek

Chen

Duclos

S

P-PSDB;

2002-723329/78. ABG96478.

New isolated nucleic acid encoding MP-1 protein, useful for preventing, treating, or ameliorating diseases associated with aberrant metalloproteinase activity, e.g. immune, metabolic, inflammatory and neurological disorders.

Claim 1; Fig 1A-C; 473pp; English.

cc metalloprotease (MP-1). (I) is useful for preventing, treating, or cc ameliorating a medical condition, particularly an immune disorder, an cc aberrant glutamate transport or motor neuron disorder; such as cc amyotrophic lateral sclerosis (ALS), its juvenile form or an ALS-like condition. The compositions and methods are also useful for diagnosing, croated with MP-1 activity, e.g. diabetes, cancer, reproductive cc disorders (e.g. Kleinfelter's syndrome, genital warts, or germinal cell caplasia), metabolic disorders (e.g. premature puberty, Kallman syndrome, cc or Cushing's syndrome), neurodegenerative diseases (Alzheimer's disease, Huntington's disease or Tourette syndrome), liver cand renal disease and immune disorders (e.g. AIDS, rheumatoid arthritis cor sepsis), pulmonary diseases (e.g. moumonia, emphysema or cystic cfibrosis) and vascular, inflammatory and neurological disorders (e.g. Alzheimer's disease or Parkinson's disease). This sequence represents a cc metalloprotease MP1 polynucleotide The invention describes an isolated nucleic acid molecule (I) encoding metalloprotease (MP-1). (I) is useful for preventing, treating, or

Sequence 2197 BP; 681 A; 441 Ç 439 <u>.</u> 636 Η, 0 Ģ 0 Other;

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                        Alignment
Pred. No.:
                               Score:
8.75e-147
1385.00
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                       Length:
Matches:
Conservative:
        Mismatches:
Indels:
2197
267
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US-10-649-273-2\_COPY\_148\_414 (1-267) × ABS76635 (1-2197)

MetGluAlaHisAlaLeuThrIleArgLeuThrAsnLysValGluPheProPheLeuVal 20

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cérebroprotective; antiparkinsonian; nootropic; antiinflammatory; antiulcer; hepatotropic; gymaecological; antibacterial; virucide; protozoacide; antiparasitii; cell proliferative disease; pMOD; protein modification and maintenance molecule; immunogenic fragment; cancer; autoimmune; inflammatury disease; neurological disorder; gastrointestinal; developmental; vesicle trafficking disorder; infection; protein-protein interaction; drug-target interaction; gene expression profile; human; gene; ds.
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**ABT23207** Gaps:

(1-2572)

Percent Similarity:
Best Local Similarity:
Query Match:

1.09e-146 1385.00 100.00% 100.00%

Conservative: Mismatches: Indels:

2572 267 0 0 0 0

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The invention relates to an isolated polypeptide comprising: any of 28 cc sequences of 48-1256 amino acids; a natural amino acid sequence at least CO 90% identical to the 28 amino acids sequences, 94% identical to a sequence co of 703 or 267 amino acids, 96% identical to a sequence of 414 amino concept of 703 or 267 amino acids, 96% identical to a sequence of 414 amino concept of 703 or 267 amino acids, 96% identical to a sequence of 414 amino concept of 703 or 267 amino acids, 96% identical to a sequence of 414 amino concept of 703 or 267 amino acids, 91% identical to a sequence of 414 amino concept of 705 or 70% identical to a sequence of 414 amino concept of 705 or 70% identical to a sequence of 422 amino acids, all given in concept of 705 or 70% identical polypeptides. The polypeptides and polymuclectides are useful concept of 705 or 70% identical polypeptides and polymuclectides are useful concept of 705 or 70% identical polypeptides, or 70% identical proliferative diseases (e.g. cancer, concept of 70% identical polypeptides, or 70% identical polypeptides, or 70% identical polypeptides, or 70% identically bind to 70% identically potein-protein for 70% identically bind to 70% identically potein-protein for 70% identically bind to 70% identically potein-protein for 70% identically bind to 70% identically potein-protein interactions, drug-target interactions, and 70% or 70% identically potein-protein interactions drug-target interactions, and 70% or 70% identically potein-protein for 70% identically bind to 70% identically 70% identically 70% identically 70% identically 70% identically 70% identically 70% identically 70% identically 70% identically 70% identically 70% identically 70% identically 70% identically 70% identically 70% identically 70% identically 70% identically 70% identically 70% identically 70% identically 70% identically 70% identically 70% identically 70% identically 70% identically 70% identically 70% identically 70% identically 70% identically 70% identically 70% identically 70% identically
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06-JUL-2001; 2001US-0303445P.
13-JUL-2001; 2001US-0305405P.
09-AUG-2001; 2001US-0311442P.
24-AUG-2001; 2001US-031821P.
29-AUG-2001; 2001US-0318992P.
03-MAY-2002; 2002US-0378205P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated human PMOD polypeptide and polynucleotide, useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant PMOD expression, e.g. cancer, AIDS, atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 91;
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Human; adenosine deaminase; seven transmembrane domain receptor; cancer; 7TM; glycoprotease; immune disorder; IgA deficiency; allergy; arrhythmia; rheumatoid arthritis; diabetes; atherosclerosis; cardiovascular disorder; hypertension; ischaemic heart disease; obesity; myocardial infarction; endothelial cell disorder; Grave's disease; psoriasis; brain disorder; Parkinson's disease; haematopoietic disorder; cerebral oedema; metabolic disorder; liver disorder; platelet disorder;
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646 20

LeuLeuIleSerGlyGlyHisCysLeuLeuAlaLeuValGlnGlyValSerAspPheLeu

Percent Similarity: Best Local Similarity:

1348.00 98.50% 97.38% 97.33%

Conservative: Mismatches: Indels: Length: Matches:

Gaps:

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CC protease or seven transmembrane domain (7TM) receptor family members. Sequences of the invention are useful in diagnosing and treating cancer (CC sequences of the invention are useful in diagnosing and treating cancer (CC lung cancer), immune disorders (e.g. selective IgA deficiency, rheumatoid (CC archritis, diabetes, allery), heart or cardiovascular disorders (e.g., colon or (CC reptorial), atherosclerosis, arrhythmias, ischaemic heart disease, (CC myocardial infarction, thrombus) including endothelial cell disorders (e.g., seoriasis, Grave's disease), haematopoietic disorders disease), (CC disorders (e.g. cerebral oedema, Parkinson's or Alzheimer's disease), (CC pain and metabolic disorders (e.g. obseity), liver disorders or platelet (e.g. diagnostic assays, prognostic assays, monitoring clinical trials (c.g., diagnostic assays, prognostic assays, monitoring clinical trials and prophylactic and therapeutic methods. The (c.g., diagnostic asiay) and prophylactic and therapeutic methods. The (c.g., diagnostic asiay) and prophylactic and therapeutic methods. The (c.g., diagnostic asiay) and prophylactic and therapeutic methods. The (c.g., diagnostic asiay) and prophylactic and therapeutic methods. The (c.g., diagnostic asiay) and prophylactic and therapeutic methods. The (c.g., diagnostic asiay) and as surrogate markers. Sequences of the invention are (c.g., 28472 cDNA)
New 38650, 28472, 5495, 65507, 81588 or 14354 nucleic acid molecules, useful for diagnosing and treating cancer, immune, cardiovascular, hematopoietic, brain, pain, metabolic, liver or platelet disorders, a
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08-NOV-2000; 2000US-0246772P.
15-NOV-2000; 2000US-0249185P.
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08-NOV-2000;
15-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                     Sequence 1820
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(KAPE/) KAPELLER-LIBERMANN
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                                                                                                                                                                                                                                                                                         Parkinson's disease; anorexia nervosa; cachexia; glycoprotease; gene; ss.
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                                                                                                                               Location/Qualifiers
                              /*tag= a
/product= "Glycoprotease 28472"
/note= "Specifically claimed in
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                                                                                                                                                                                                                                                                                                                                               Score:
                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention describes isolated 38650, 28472, 5495, 65507, 81588 and CC 14354 nucleic acid molecules (I) and their encoded polypeptides (II). The C38650 nucleic acid molecule comprises a sequence encoding adenosine CC deaminase. The 28472 nucleic acid molecule comprises a sequence encoding CC a human glycoprotease. The 5495, 65507, 81588 and 14354 comprise CC 38650, 28472, 5495, 65507, 81588 or 14354 nucleic acid and polypeptide CC sequences that encode a human seven transmembrane domain (77M). The CC sequences are useful for diagnosing, preventing or treating a subject CC with or at risk of developing a disorder, e.g. cancer or aberrant CC cellular proliferation and/or differentiation (e.g. breast, ovarian, CC prostate, colon or lung cancer), immune disorders, heart disorders, CC cardiovascular disorders, endothelial disorders, heart disorders, CC liver disorders or platelet disorders, pain and metabolic disorders, CC liver disorders or platelet disorders. These disorders include carcinoma, Sarcoma, leukaemia, Hodgkin's disease, autoimune disorders, CC ischaemia, heart disease, Crohn's disease, autoimune disorders, CC ischaemia, parand's disease, aneurysm, cerebral ischaemia, peripheral CC cachexia or diabetes. This sequence encodes the novel human glycoprotease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New adenosine deaminase, glycoprotease and seven transmembrane domain nucleic acids and polypeptides, designated 38650, 28472, 5495, 65507, 81588 and 14354, useful for treating e.g. leukemias, Hodgkin's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-NOV-2000; 2000US-0246768P.
08-NOV-2000; 2000US-0246772P.
15-NOV-2000; 2000US-0249185P.
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                                                                                                           LeuLeuGlyLysSerLeuAspIleAlaProGlyAspMetLeuAspLysValAlaAargArg
LeuSerLeuIleLysHisProGluCysSerThrMetSerGlyGlyLysAlaIleGluHis
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               Iscgai T, Sugiyama T,
Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
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24-JAN-2002; 2002US-0350435P.
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              Otsuki T, Wakamatsu A, Sato H, Hio Y, Otsuka K, Nagai K, Irie Otsuka M, Nagahari K, Masuho Y;
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New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases in which the gene is involved, or as target molecules for gene therapy.

The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.

T; 0 U; 0 Other;

ASDCYSASDPheSerPheThrGlyLeuGlnHisValThrASDLYSIleIleMetLySLYS TGTAAGCAGAGACTTGTTACCTCAAAATAATGCAGTACTGGTTGCATCTGGTGGTGTC CysiysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyVal ThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeuPhe GAAAAAGAGGAAGGTATTGAGAAGGGGCAAATCCTGTCTTCAGCAGCAGACATTGCTGCC GluLysGluGluGlyIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAla LeuAlaLysGlnGlyAsnArgPheHisPheAspIleLysProProLeuHisHisAlaLys LeuLeuGlyLysSerLeuAspIleAlaProGlyAspMetLeuAspLysValAlaArgArg CTTTTGATTTCTGGAGGTCACTGTCTGTTGGCATTAGTTCAAGGAGTTTTCAGATTTTCTG LeuLeuIleSerGlyGlyHisCysLeuLeuAlaLeuValGlnGlyValSerAspPheLeu **ACAGTACAGCACAATGGCATGTCATCTTGTGAAAAGAACACATCGGGCTATTCTGTTT** TTGGCCAAACAAGGAAATAGATTTCATTTTGACATCAAACCTCCCTTGCATCATGCTAAA CTTCTTGGAAAGTCTTTGGACATAGCACCAGGTGACATGCTTGACAAGGTGGCAAGAAGA Length: Matches: Conservative: Mismatches: Indels: (1-2208)1324 180 1264 160 1204 140 1144 1084 100 1024 1384 200 120 80 1435 220 60 964 904 40 844 20

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Alignment Scores:
                                 US-10-649-273-2_COPY_148_414 (1-267) x ADQ24627 (1-2890)
                                                                                                                   Percent Similarity:
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                                                                                                Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2;
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89.51%
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                                                               Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                              diagnostic and therapeutic polynucleotide; dithp; antiarteriosclerotic; antiinflammatory; cerebroprotective; antiinflammatory; cerebroprotective; nontropic; antidiabetic; immunosuppressive; neuroprotective; nortropic; neuroleptic; tranquilizer; osteopathic; antiarthritic; antiirheumatic; cytostatic; hepatotropic; virucide; haemostatic; anti-HIV; antithyroid; thyromimetic;
 gene therapy; protein replacement therapy;
                  dermatological; antibacterial; fungicide; antiparasitic; anticonvulsant;
thrombolytic; anticoagulant; anorectic; vasotropic; antiulcer;
                                                                                                                                               Human diagnostic and therapeutic polynucleotide (dithp), SEQ ID No 100.
                                                                                                                                                                               29-JAN-2004
                                                                                                                                                                                                               ADE31345;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyVal
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Homo

sapiens.

WO2003062376-A2

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CC antiatteriosclerotic, antiinflammatory, cerebroprotective, antilipaemic, antidiabetic, immunosuppressive, neuroprotective, notropic, neuroleptic, cranquilizer, osteopathic, antiarthrithc, antirheumatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, cytostatic, virucide, haemostatic, anti-Hry, antithyroid, thyromimetic, cytostatic, anti-Hry, antithyroid, thyromimetic, cytostatic, cytostatic, cytostatic, anti-Hry, antithyroid, thyromimetic, cytostatic, cy
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Peralta CH, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human diagnostic and therapeutic polynucleotides and polypeptides, useful for diagnosing, treating or preventing e.g. leukemia, brain cancer, atherosclerosis, AIDS, thyroiditis, infections, obesity, stroke
                                           polynucleotide sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               comprising a naturally occurring polynucleotide sequence at least 90% identical to the dithp polynucleotide; a polynucleotide complementary to the dithp polynucleotide or its polynucleotide which is at least 90% identical; or an RNA equivalent of any of the polynucleotides mentioned above. The dithp polynucleotides have the following activities:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-JAN-2002; 2002US-0349384P.
17-JAN-2002; 2002US-0349413P.
17-JAN-2002; 2002US-0349946P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel isolated human diagnostic and therapeutic polynucleotide (designated dithp). The novel dithp polynucleotide comprises: any of 188 DNA sequences consisting obase pairs fully defined in the specification; a polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or Alzheimer's.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; SEQ ID NO
BP; 1105 A;
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Lan RY, Urashka ME;
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Ç;
0 Other
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Alignment Scores:

-	Db 2169 CCTTTGCATCTTTTCGTTTCACAGTATTTAAT	Qy 54	sequences Db 2229 GTATAGCATGTTTTATTCATTCAGGGGTTTTT
	2169 CCTTTGCATCTTTTCGTTTCACAGTATTTAATTTTATGACTCTAAAAAATATGTTTCTTT :	54Leu !	2229 GTATAGCATGTTTTAFTCATTCAGGGGTTTTTTGTTTTGT

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ATCATAAGGAACAGGGTTGTCTGCTTACCTGAATATCAGCTATAGTCTATATTTTGCCAAA 2230

CCAACCAATAGAAGAGCAAACATAGACAGGGGCAGTGATTGGCCTCTTATTGTTCGGGTC 2290

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2349

2409

ACAAGTTCTTATTATTGACGTTCATCATTAAGCAGTTATTGTCAACTTCAAGCCCCATTTT

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ATAGGAAACTACAACAACAACGACACGTGCTTCCCACAGTGAAATAATAGGAAGTATAGG 2410

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CAGACAGGGTCCCCCCCCACCCCCCTTTGTTTTTAGAATACTACAGAGGCTACTGCCATAT 2470

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GTACACGAATTTATAATTCTTAGCCTTTCTTAATAAAATGGTAAGAGGTTCATATCTGTA 2710

TTTTATCTTAGTAAACTGAACACAAAATTCACATATGGTGAGAAAAAAATAGAAAGCAGTA 2770

TGTCCATTTCAACTAAGTAGCAATAGATGTGCTACCACCATTCACCTAAATATTTCTGAA 2830

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CCAGGTGACATGCGTTGACAAGGTAATTAAGAATTAATTTCTCCATTCTTTTTTGTTATGT 2890

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TGGGCATTAGTTCAAGGAGTTTCAGATTTTCTGCTTCTTGGAAAGTC-TTGGACATAGCA LeuAlaLeuValGlnGlyValSerAspPheLeuLeuGlyLysSerLeuAspIleAla 49

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US-10-649-273-2\_COPY\_148\_414 (1-267)

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3067 GTGACCAATAAAGTAGAATTTCCTTTTTTAGTTCT-TTGATTTCTGGAGGTCACTGTCTG

LeuThrAsnLysValGluPheProPheLeuValLeuLeuIleSerGlyGlyHisCysLeu

Percent Similarity:
Best Local Similarity:
Query Match:

2.99e-102 995.50 44.82% 44.64% 71.88%

Conservative: Mismatches: Indels:

Length: Matches:

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RESULT 12
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ID ABQ75
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06-DEC-2000; 2000US-0251803P.
06-DEC-2000; 2000US-0251820P.
                                                                                                                                      Murine; mouse; protease; calcium activated neutral protease type 5; CAPN5; tryptase 4; sialoglycoprotease; enzyme; genetic disease; neurological; neuropsychological; psychotic illness; transgenic animal;
                                   05-DEC-2001; 2001WO-US046405
                                                                                 WO200245491-A2
                                                                                                        Mus musculus
                                                                                                                              gene;
                                                                                                                                                                                     Murine sialoglycoprotease-like gene sequence SEQ ID NO:7.
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Novel transgenic animal, comprising a disruption in protease target gene, is useful for identifying agents that ameliorates a phenotype associated with a disruption in a protease target gene.
                                                                                                                                                          Example 3; Fig 7; 62pp; English.
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                                                                                                                                                                                                                              (DELT-) DELTAGEN INC.
                                                                                                                                                                                                   2002-657389/70
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The present invention describes a non-human transgenic animal (I) C comprising a disruption in a protease target gene (PG) selected from CC calcium activated neutral protease type 5 (CAPN5) gene, tryptase 4 gene CC and sialoglycoprotease-like gene. Also described is a targeting construct (II), comprising a first polynucleotide sequence homologous to at least a CC first portion of PG, a second polynucleotide sequence homologous to at CC least a second portion of PG and a selectable marker. (II) is useful for CC producing a transgenic mouse comprising a disruption in a protease target gene, by introducing (II) into a cell, introducing the cell into a CC blastocyst, implanting the resulting blastocyst into a pseudopregnant CC gene, where the pseudopregnant mouse gives birth to a chimeric mouse, CC and breeding the chimeric mouse to produce the transgenic mouse. (I) is constituted for identifying an agent that modulates the expression or function of a protease target gene, by administering an agent to (I) and CC determining whether the expression or function of the disrupted protease target gene by administering an agent to (I) and CC consected gene in (I) is modulated. (I) is also useful for testing the efficacy of proposed genetic and pharmacological therapies for human CC genetic diseases, such as neurological, neuropsychological or psychotic illness. The present sequence represents murine sialoglycoprotease-like gene sequence, which is used in an example from the present invention

Sequence 1572 BP; 459 A; 337 C; 340 G; 429 T; 0 U; 7 Other;

Alignment Scores: Pred. No.:

Score:

Query Match:

Percent Similarity: Best Local Similarity:

2.67e-101 983.00 84.21% 78.95% 70.97%

Length:
Matches:
Conservative:
Mismatches:
Indels:

Gaps:

(1-1572)

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                                    TTGGCCAAAGACGGAAATAGATTCCATTTTACTATCAATCCACCTATGCAGAATGCTAAG
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                                                                                                                                                                                                                                                                                                                    MetGluAlaHisAlaLeuThrIleArgLeuThrAsnLysValGluPheProPheLeuVal
                                                                                                                   LeuAlaLysGlnGlyAsnArgPheHisPheAspIleLysProProLeuHisHisAlaLys 100
                                                                                                                                              CTTTCTTTAATCAAACATCCAGAATGTTCTACAATGAGTGGTGGAAAAGCTATAGAACAG
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RESULT 13
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as mybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed
                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful diagnostics, forensics, gene mapping, identification of mutat responsible for genetic disorders or other traits and to asse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cc genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is cuseful for generating antibodies against it, detecting or quantitating a cc useful for generating antibodies against it, detecting or quantitating a cc polypeptide in tissue, as molecular weight markers and as a food cc supplement. (II) and its binding partners are useful in medical imaging co f sites expressing (II). (I) and (II) are useful for treating disorders involving abservant protein expression or biological activity. The cc quantity and polynucleotide sequences have applications in cc diagnostics, forensics, gene mapping, identification of mutations cc responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and camino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this cateful did not appear in the printed specification, but was obtained in celectronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                  GACATAGAAGGCATCCGCTATGAACCAAAGTATGTGGCTCCTTCAGGGCTG
                                                                                                   AspIleGluGlyIleArgTyrGluProLys-----CysProLeuGlyVal 247
                                                                                                                                               GlyIleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeuGlyIleLeuHis
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                                                                                                                                                                                                                                                                                                                                                                                                                        self renewing multipotent progenitors (MPPs), common lymphoid progenitors (CLPs) and common myeloid progenitors (CMPs), which are collectively referred to as bone marrow stem cells populations. As such, these methods can be used to identify associated multi-lineage affiliated genes and hence the underlying molecular mechanisms in physiological haematopoietic development. This polynucleotide sequence is DNA associated with a murine MPP sub population of cells of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Classifying an unknown multi-lineage affiliated gene comprises isolating expressed nucleic acid sequences from the discrete cell sub-populations.
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                                                              SerGlyGlyValAlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAla 196
                                                                                                          GCTATTCTGTTTTGCAAGCAGAGAAATTTGCTCTCTCCAGCTAACGCAGTATTAGTTGTA
                                                                                                                                     AlaIleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAla 176
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                                                                        hence the underlying molecular mechanisms in physiological haematopoietic development. This polynucleotide sequence is DNA associated with a murine
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US-10-649-273-2_COPY_148_414 (1-267) x ADL86726 (1-371)
Search completed: February 16, 2005, 13:58:48 Job time: 525.461 secs
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                                                                                                                   197 ThrGlnCysThrLeuLeuCysProProProArgLeuCysThrAspAsnGlyIleMetIle 216
                                                                                                                                                                                                  137 AspIleAlaAlaThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArg 156
                                                    257 SerIleLys 259
                                                                                                                                                                                                                                          157 AlaIleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAla 176
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Result
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-Q=/Cgn2 1/USPTO, spool/USI0649273/runat 14022005 114704 16425/app query.fasta_1.1429
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-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALICM=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WARIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=30 -WARN TIMEOUT=30 -THREADS=1 -XGAPDP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum DB seq length: 2000000000
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-MODEL=frame+_p2n.model -DEV=xlh
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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                   US-09-774-528-177
US-10-067-443-23
US-10-067-443-21
US-10-067-443-21
US-10-067-443-20
US-09-596-002-38
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US-09-591A-804
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Sequence 177, App
Sequence 23, Appl
Sequence 1, Appli
Sequence 21, Appl
Sequence 20, Appl
Sequence 806, App
Sequence 806, App
Sequence 801, App
Sequence 1, Appli
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## ALIGNMENTS

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RESULT 1
US-09-774-528-177
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                                                                                                            PILE REFERENCE: 802
CURRENT APPLICATION NUMBER: US/09/774,528
CURRENT FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 441
SOFTWARE: pt FL genes Version 2.0
SEQ ID NO 177
SEQ ID NO 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 177, Application US/09774528 Patent No. 6743619
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APPLICANT:
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APPLICANT:
           LENGTH: 1416
TYPE: DNA
ORGANISM: Homo E
FEATURE:
NAME/KEY: CDS
LOCATION: (205)
                                                                                                                                                                                                    APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6743619el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                      Zhang, Jie
Zhao, Qing A.
Yang, Yonghong
Xue, Aidong J.
Wehrman, Tom
Wang, Jian-Rui
Wang, Dunrui
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Zhou, Ping
Goodrich, Ryle
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Asundi, Vinod
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Alignment Scores:

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Percent Similarity:
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Query Match:
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Sequence 23, Application US/10067443
Patent No. 6642041
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE
TITLE OF INVENTION: SPINAL CORD, MP-1
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                                                                                           CCACAATTAAAAATGGAGATA
                                                                                                                               ProLysCysProLeuGlyValAspIleSerLysGluValGlyGluAlaSerIleLysVal
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Matches:
Conservative:
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              EXPRESSED
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CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.0
SEQ ID NO 23
LENGTH: 1526
TYPE: DNA
ORGANISM: homo sapiens
US-10-067-443-23
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Best Local Similarity:
Query Match:
DB:
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                                                  AlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThr
                                                                                                                              ThrvalGlnHisThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeuPhe
                                                                                                                                                                                                            GluLysGluGluGlyIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAla 140
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                        IleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAspIleGluGlyIleArgTyrGlu
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APPLICANT: Bristol-Myers Squibb Company
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
PILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
NUMBER OF SEQ ID NOS: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 2197
TYPE: DNA
ORGANIEM: Homo sapiens
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Patent No. 6642041
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                              GluLysGluGluGlyIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAla 140
                                                                                                      AsnCysAspPheSerPheThrGlyLeuGlnHisValThrAspLysIleIleMetLysLys 120
                                                                                                                                                                 LeuAlaLysGlnGlyAsnArgPheHisPheAspIleLysProProLeuHisHisAlaLys 100
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ThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeuPhe 160
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; SEQ ID NO 21
; LENGTH: 1387
; TYPE: DNA
; ORGANISM: homo sapiens
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LeuSerLeuIleLysHisProGluCysSerThrMetSerGlyGlyLysAlaIleGluHis 80
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Matches:
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Mismatches:
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GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR PILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
NUMBER OF SEQ ID NOS: 71
                                                                                                                                                                                                                           1 MetGluAlaHisAlaLeuThrIleArgLeuThrAsnLysValGluPheProPheLeuVal
                                                                                                                                         21 LeuLeuIleSerGlyGlyHisCysLeuLeuAlaLeuValGlnGlyValSerAspPheLeu 40
                       CTTTTGATTTCTGGAGGTCACTGTCTGTTGGCATTAGTTCAAGGAGTTTCAGATTTTCTG
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Oy 58	Allgament Scores: 1.34e-99 Length: 14364 Pred. No.: 1.34e-99 Length: 240 , Score: 824.50 Matches: 240
Db 11744 TTTTGTTTTGTTAGTAATTTTCAATTTATTTCCTTTGCATCTTTTCGTTTCACAGTATTT 11803	11: 14: 15: 15: 15: 15: 15: 15: 15: 15: 15: 15
Qy 57 57	ORGANI
Db 11684 TGAATATCAGCTATAGTCTATATTTGCCAAAGTATAGCATGTTTTATTCATTC	FUNCTION 14364
Qy 57 57	SOFTWARE: PatentIn
Db 11624 GGGCAGTGATTGGCCTCTTATTGTTCGGGTCATCATAAGGAACAGGGTTGTCTGCTTACC 11683	FRIOR FILLING DATE: 2001-04-10  : NUMBER OF SEO ID NOS: 71
Qy 57 57	05
Db 11564 AAGCAGTTATTGTCAACTTCAAGCCCATTTTCCAACCAATAGAAGAGCAAACATAGACAG 11623	05
Qy 57 57	FILE REPERENCE: DOOTS NE FILE REPERENCE: DOOTS NE FILE REPERENCE: DOOTS NE
Db 11504 CTTCCCACAGTGAAATAATAGGAAGTATAGGACAAGTTCTTATTATTGACGTTCATCATT 11563	; APPLICANT: BISIOL-MYSES SQUIDE COMPANY ; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED I ; TITLE OF INVENTION: COINT, COEN MD-1
Qy 57 57	GENERAL INFORMATION:
Db 11444 AATACTACAGAGGCTACTGCCATATATAGGAAAACAAACA	0.14
11384 TTAAATCACACAATTACTTACACCACAGACAGGGTCCCCCCCC	Db 1305 GCTTCCATAAAAGTACCACAATTAAAAATGGAGATA 1340
Qy 57 57	Qy 256 AlaSerIleLysValProGlnLeuLysMetGluIle 267
Db 11324 GGTAAAATAAGAGAATATATATAGATTAACATAAGGACATTAAAGATGCAATGCACAGAA 11383	Db 1245 GGCATCCGCTATGAACCAAAATGTCCTCTTGGAGTAGACATATCAAAAGAAGTTGGAGAA 1304
Qy . 57 57	Qy 236 GlyIleArgTyrGluProLysCysProLeuGlyValAspIleSerLysGluValGlyGlu 255
Db 11264 TATTTTGCCAAATAATGTATGTGAAAGAACGTGCTTCGTAAACTAACATACTGCAAAAAA 11323	Db 1185 ATTGCATGGAATGGTATTGAAAGACTACGTGGTGGTGGCATTTTACATGACATAGAA 1244
Qy 57 57	Oy 216 IleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAspIleGlu 235
Db 11204 AAATGGTAAGAGGTTCATATCTGTACATAAAGGCTGAAATAGTTTGCAGATACAGTTATG 11263	Db 1125 GCAACACAGTGCACTTTGTGTGTCCTCCTCCCAGACTATGCACTGATAATGGCATTATG 1184
Qy 57 57	Qy 196 AlaThrGlnCysThrLeuLeuCysProProProProArgLeuCysThrAspAsnGlyIleMet 215
Db 11144 ATGGTGAGAAAAATAGAAAGAGTAGTACACAATTTTATAATTCTTAGCCTTTCTTAATA 11203	Db 1065 GCATCTGGTGGTCGCAAGTAACTTCTATATCCGCAGAGCTCTGGAAATTTTAACAAAC 1124
Qy 57 57	Qy 176 AlaSerGlyGlyValAlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsn 195
Db 11084 TACCACCATTCACCTAAATATTTCTGAATTTTATCTTAGTAAAACTTGAAAAAAATTCACAT 11143	Qy 156 ArgAlaIleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuVal 175
Db 11024 TTAATTTCTCCATTCTTTTTTGTTATGTTGTCCATTTCAACTAAGTAGCAATAGATGTGC 11083	Db 945 GCAGACATTGCTGCCACAGTACAGCACAATGGCATGTCATCTTGTGAAAAGAACACAT 1004
Qy 57 57	Qy 136 AlaAspileAlaAlaThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHis 155
Qy 41 LeuLeuGlyLysSerLeuAspIleAlaProGlyAspMetLeuAspLysVal 57	Qy 127
10905 CTTTGATTTCTGGAGGTCACTGTCTGTGGCATTAGTTCAAGGAGTTTCAGATTTCTG	
21 LeuLeuIleSerGlyGlyHisCysLeuLeuAlaLeuValGlnGlyValSerAspPheLeu	121 GluLysGluGlyIle
Qy 1 MetGluAlaHiBAlaLeuThrIleArgLeuThrAsnLysValGluPheProPheLeuVal 20 	Qy 101 AsnCysAspPheSerPheThrGlyLeuGlnHisValThrAspLysIleIleMetLysLys 120
US-10-649-273-2_COPY_148_414 (1-267) x US-10-067-443-20 (1-14364)	Db 705 TTGGCCAAACAAGGAAATTCATTTTGACATCAAACCTCCCTTGCATCATGCTAAA 764
Percent Similarity: 26.73% Conservative: 0 Best Local Similarity: 26.73% Mismatches: 2 Query Match: 59.53% Indels: 657 DB: 4 Gaps: 4	Db 645 CTTTCTTAATAAACATCCAGAGTGCTCCACCATGAGTGGGAAAGCCATAGAGCAT 704  Qy 81 LeuAlaLysGlnGlyAsnArgPheHisPheAsplleLysProProLeuHisHisAlaLys 100

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TAAATGGTAGTAATTCATAGATGGAATTTTACATGGATATCAAAGAATAATTTTTTCAGA 1	174	65 LyshisproglucysserThrmetSerGlyGlyLysAlaIleGluHisLeuAlaLysGln 84
Alignment Scores:  Pred. No.:  9.21e-20  Score:  Score:  94750  Matches:  Percent Similarity:  49.61*  Best Local Similarity:  33.98*  Query Match:  22.27*  Indels:  94750  Matches:  94750  Matches:  97  Matches:  98  Mismatches:  101  Ouery Match:  22.27*  Indels:  99  Percent Similarity:  94750  Matches:  97  Matches:  97  Mismatches:  101	RESULT 6 US-09-596-002-38 US-09-596-002-38  (US-09-596-002-38  (Sequence 38, Application US/09596002  Patent No. 6632636  (PATENT NOTERNATION:  APPLICANT:  APPLICANT:  APPLICANT:  PATENTION:  PATENT:  PATENTA  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:  PATENTION:	174

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# Sequence 806, Application US/09540236

# Patent No. 6673910

# GENERAL INFORMATION:

# APPLICANT: Gary L. Breton et al.

# TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELITITE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

# TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

# TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

# TITLE OF INVENTION: NUMBER: US/09/540,236

# CURRENT APPLICATION NUMBER: US/09/540,236

## CURRENT APPLICATION NUMBER: US/09/540,236

## CURRENT FILING DATE: 2000-04-04

## NUMBER OF SEQ ID NOS: 3840

## SEQ ID NO 806

## LENGTH: 1053

## TYPE: DNA

## ORGANISM: M.catarrhalis

## US-09-540-236-806
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Best Local Similarity:
Query Match:
                                                                                                 US-09-252-991A-884/c
; Sequence 884, Application US/09252991A
; Patent No. 6551795
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                                                                                        GENERAL INFORMATION:
   APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
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Matches:
Conservative:
Mismatches:
Indels:
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US-10-649-273-2_COPY_148_414 (1-267) x US-09-540-236-806 (1-1053)
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US-09-252-991A-884
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PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 884
LENGTH: 1059
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57
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                             GluProLysCysProLeu 245
                                                                                                                                  CAGGTGTTCTACGCCCGCCCCCCCCCTTCTGCACCGACAATGGCGCGATGATCGCCTTACGCC 109
CAGCCGCGCTGGCCGATG 40
                                                                                      GlyIleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAspIleGluGlyIleArgTyr 239
||| ;::||||||
                                                                                                                                                       ThrLeuLeuCysProProProArgLeuCysThrAspAsnGlyIleMetIleAlaTrpAsn 219
                                                                                                                                                                                                                                    ValAlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCys 199
                                                                                                                                                                                                                                                                       -----AAGCAGACCGGCCTG-----AAGAAC-----CTGGTGATCGCCGGCGGT
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                                                                  GGCTGCCAGCGCCTGCTCGCCGGC---
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SEQ ID NO 801
LENGTH: 1206
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
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ĠŢĊAGCGCCĂĂĊCAGGCGCTGĊĠĊAGCGGCĊŢĠĠĂĂAAGATGCTCGGCGAAATGAAGGGG
                                       ValAlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCys 199
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                                                                                                                           PheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGly 179
                                                                                                                                                                       CTGGCGTTCCAGACCGCGGTGGTCGAGACCCTGCTGATCAAGTGCCGTCGCGCCTTG---
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; Sequence 1, Application US/09557884
; Patent No. 6506581
; GENERAL INFORMATION:
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MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION NOMBER: US/09/557,884
FILING DATE: 25-Apr-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: MICHAELE S. MAR'S
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-109-8504
                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1117
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                         20
GlyIleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAspIleGluGlyIleArgTyr 239
                                                                ATGGAAGGGCATTTACTTGCGCCAATGCTTGATGACAATTCACCGCACTTTCCTTTTGTT 552822
                                                                                                       MetGluAlaHisAlaLeuThrIleArgLeu---ThrAsnLysValGluPheProPheLeu
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COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGGTGTTCTACGCCCGCGCGCTTCTGCACCGACAATGGCGCGATGATCGCCTACGCC 1116
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US-09-643-990A-1/c
y Sequence 1, Application U
patent No. 6528289
GENERAL INFORMATION:
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                     ZIP: 20850
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPER: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE ASCII Text
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/643,990A
FILING DATE: 23-AUG-2000
CLASSIFICATION: «Unknown»
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                                                                                                                                                                                                                                                                                                                                                                        J. Craig Venter
TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae
Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEB: Human Genome Scie
STREET: 9410 Key West Avenue
    PRIOR
                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyGlyValAlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThr 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---ATTAAATGTAAG---CGTGCATTGAAAGAAACAGGCTATAAACGTTTAGTGATTGCG 552402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCAATTAAAAACGAGGGCGAACTGATAGAGCAA------ACTAAAGCAGAT 552498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LysGluLysGluGluGly-----IleGluLysGlyGlnIleLeuSerSerAlaAlaAsp 137
                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                        STATE: MD
                                                                                                                                                                                                                                                                             CITY: Rockville,
    APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Owen White
Hamilton O. Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mark D.
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APPLICATION NUMBER: 08/487,429 FILING DATE: 1995-06-07

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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-649-273-2_COPY_148_414 (1-267) x US-09-643-990A-1 (1-1830121)
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186P1C1
TELEPHONE: 301-610-5790
TELEPAX: 310-309-8439
552341 GGTGGCGAAGTGTTTTATCCTCAACCTCAATTTTĞTÄCAĞATAATGGTGCGATĞATTĞCT 552282
                                                                                                                                                                                                                                                                                                                                                      552542 GCAATTAAAAACGAGGGCGAACTGATAGAGCAA------ACTAAAGCAGAT 552498
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                                                                                  GlyGlyValAlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThr 197
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GGAGGGGTGAGCGCAAATAAAAAACTCCGAGAAAACGCTTGCGCACTTAATGCAAAATTTA 552342
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                         GlnCysThrLeuLeuCysProProProArgLeuCysThrAspAsnGlyIleMetIleAla 217
                                                                                                                                                                                                            IleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSer 177
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                    ATTGCTTATGCTTTCCAAGATGCGGTGGTGGATACTCTTGCC-------
                                                                                                                                                                                                                                                                                                           IleAlaAlaThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArgAla 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LysAsnCysAspPheSerPheThrGlyLeuGlnHisValThrAspLysIleIleMetLys 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HisLeuAlaLysGlnGlyAsnArgPheHisPheAspIleLysProProLeuHisHisAla 99
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Matches:
Conservative:
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APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Wiegand, Roger C.

FITLE OF INVENTION: Myxococcus xanthus Genome Sec FILE REFERENCE: 38-10 (15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 6612

LENGTH: 996

TYPE: DNA

ORGANISM: Myxococcus xanthus

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          552281 TACACAĞĞİTTTTTACĞİİTÂAAACAAĞĞİ
                                                                                                                                                    646 GCGGTGCTGCACGTGCAGAAGCACGGCGTGCCGCAGGGGGCAGGCCCTG-----
                                                                                                                136
                                                                                                                                                                               116 IleIleMetLysLysGluLysGluGlyIleGluLysGlyGlnIleLeuSerSerAla
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                                                                                                                                                                                                                                                                                                                                                                                            514 ATCCTCGGCCTG---CCGTATCCG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetGluAlaHisAlaLeuThrIleArgLeuThrAsnLysVal---GluPheProPheLeu
                                                                                                                                                                                                                                                                                                                                    HisLeuAlaLysGlnGlyAsn------ArgPheHisPheAspIleLysProPro 95
                                  ArgAlaIleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuVal 175
                                                                                                                AlaAspIleAlaAlaThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHis
                                                                                                                                                                                                                                 GCGCTGCCGGGCGACAACTTCGACGTGTCCTTCTCCGGGTTGAAG
                                                                                                                                                                                                                                                                     LeuHisHisAlaLysAsnCysAspPheSerPheThrGlyLeuGlnHisValThrAspLys 115
                                                                                                                                                                                                                                                                                                               CAGTTGGCGCAGCAGGGGAACCCCGGAGGCCATCCGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                            ArgLeuSerLeuIleLysHisProGluCysSerThrMetSerGlyGlyLysAlaIleGlu 79
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
SEQ ID NO 503
LENGTH: 2582
TYPE: DNA
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  AlaAspIleAlaAlaThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHis 155
                                             GCGGTGCTGCACCACGTGCAGAAGCACGGCGTGCCGCAGGGGGAGGCGCTG-----
                                                                                     IleIleMetLysGysGluLysGluGlyIleGluLysGlyGlnIleLeuSerSerAla 135
                                                                                                                                                                      LeuHisHisAlaLysAsnCysAspPheSerPheThrGlyLeuGlnHisValThrAspLys 115
                                                                                                                                                                                                                    CAGTTGGCGCAGCAGGGGAACCCGGAGGCCATCCGCTTC
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TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR FILING DATE: 1900-04-05
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID 0.2341
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ORGANISM: Proteus
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664 CCCGGACTCGÁCTTTÁGTTTCTCTGGŤTTÁAAAACCTTTGCCGCTAATACTATTCGTCAA 723
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                             LysAsnCysAspPheSerPheThrGlyLeuGlnHisValThrAspLysIleIleMetLys 119
                                                                      HisLeuAlaLysGlnGlyAsnArgPheHisPheAspIleLysProProLeuHisHisAla
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Patent No. 5543312
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APPLICANT: Mellors, Alan
APPLICANT: Lo, Reggie Y.C.
APPLICANT: Abdullah, Khalid M.
TITLE OF INVENTION: Pasteurella Haemolytica
TITLE OF INVENTION: Glycoprotease
TITLE OF INVENTION: Gene and the Purified Enzyme
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,797
FILING DATE: 14-UUL1993
CLASSIFICATION: 435
                                                                                                                                                               TELEFAX: 704 334 2014 INFORMATION FOR SEQ ID NO:
TOPOLOGY: 1ii
MCLECULE TYPE:
HYPOTHETICAL: 1
ANTI-SENSE: NO
                                                                                                                                                                                                   NAME: Layton, Jr., Samuel G.
REGISTRATION NUMBER: 22807
REFERENCE/DOCKET NUMBER: 337
TELECOMMUNICATION INFORMATION:
TELEPHONE: 704 377 1561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Seltzer, Park & Gibson, P.A. STREET: 1211 Bast Morehead Street,
                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                         LENGTH: 1315 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                             TELEPHONE: 70% J. 2014
704 334 2014
707 TD NO:
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STATE: No. 5543312th Carolina
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 AlaThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeu 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGGAAGTGTTTTATGCTCGCCCTGAGTTATGTACCGATAATGGTGCCATGATTGCTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CysThrLeuLeuCysProProProArgLeuCysThrAspAsnGlyIleMetIleAlaTrp 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08087797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCGGGGATGATCCGTTTTAAAGGTGGTACCGAGGGGCCTTTA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AsnGlyIleGluArgLeuArgAlaGlyLeu---GlyIleLeuHisAspIleGluGlyIle 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |||||||:::::||||
GCGTAAGTGCTAACCGTACTTTACGCGCCAAAATGGCGATGATAATGGAACAACTCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlyValAlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGln 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PheCysLysGlnArgAspLeuLeuProGlnAsnAsn---AlaValLeuValAlaSerGly 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGTGCTTTTGAAGATGCCGTAGTAGATACTTTGGCAATAAAATGTCGTCGAGCA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACGATGATTCAGAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ArgTyrGluProLysCysProLeu 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  United States
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                                                                                                                                                                                                                                               3374-80
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                                                                                                                                                                                                                                                                                                                                                                                                             Version
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Best Local Similarity:
Query Match:
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; LOCATION:
US-08-087-797-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score:
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1080 GECTTTCTTCGCTTAAAA 109
                                                                        1020 GAAGTATTCTACCCTCGCCCACAATTTTGCACTGACAACGGCGCAATGATTGCCTACACT 1079
                                                                                                                                                                                                                        903 AAATGCAAG----CGAGCGTTAGAGCGAAACCGGCTATAAACGCTTAGTAATGGCAGGCGGC
                                  220 GlyIleGluArgLeuArg 225
                                                                                                                                                                                180 ValAlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCys 199
                                                                                                                                                                                                                                                                                                  864 CACGCATTCCAACAAGCCGTG------
                                                                                                                                                                                                                                                                                                                                   140 AlaThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeu 159
                                                                                                                                                                                                                                                                                                                                                                                                            120 LysGluLysGluGluGlyIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIleAla 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                  753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               654 CTACTCGGTTTG---GATTACCCT--------GCCGGTGTAGCGATGTCA 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      594 GAACTACTCGGGGAATCAATTGATGATGCTGCCGGTGAAGCCTTTGACAAAACAGGCAAA 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 534 GCATTATTGATTTCAGGTGGACACACCCAACTGGTAAAAGTTGACGGCGTTGGGCAATAC 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        474 ATGGAAGGGCATTTACTTGCCCCCAATGTTGGAAGAAAATGCCCCCTGAATTTCCGTTTGTG
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                                                                                                                                       |||:::::|||
|GTAAGTGCCAATAAACAATTACGAGCAGACCTTGCGGAAATGATGAAAAAATTAAAAGGC 1019
                                                                                                                                                                                                                                                        PheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGly 179
                                                                                                                                                                                                                                                                                                                                                                       AATCTTAATGAAAATGGTGAACTCGATGAGCAA-----ACCAAATGCGATATTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAATTÄGCCGAATCCGGCACGCCAAATCGTTTTAAATTCCCTCGTCCAATGACCGACAGA 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HisLeuAlaLysGlnGlyAsnArgPheHisPheAspIleLysProProLeuHisHisAla 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ArgLeuSerLeuIleLysHisProGluCysSerThrMetSerGlyGlyLysAlaIleGlu 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuLeuLeuGlyLysSerLeuAspIleAlaProGlyAspMetLeuAspLysValAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                CCGGGACTGGATTTCAGTTTCTCCGGTTTAAAAACCTTTGCTGCGAATACGATTAAAGCC 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141..1115
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270.50
46.46%
34.96%
19.53%
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps:
                                                                                                                                                                                                                                                                                                -----GTTGATACTATTTAATT
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19
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Search completed: February 16, Job time : 1648.75 secs

2005, 22:15:40

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -Q=/cgn2 1/USPTO spool/US1649273/runat 14022005 114706 16497/app query.fasta 1.1429
-Q=/cgn2 1/USPTO spool/US16649273/runat 14022005 114706 16497/app query.fasta 1.1429
-DB=Published Applications NA -OPMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=200000000 -USER=US10649273 @CCN 1 1 1053 @TUNAT 14022005 114706 16497
-MCXIEN=2000000000 -USER=US10649273 @CCN 1 1 1053 @TUNAT 1-DSPBLOCK=100
-NORUG=6 -TCPU=3 -NO MMAP -LARGGUCERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -MODEL=frame+_p2n.model -DEV=xlh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OM protein - nucleic search, using frame_plus_p2n model
                      Published Applications NA:*

1: /cgn2_6/ptcdata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptcdata/2/pubpna/US06_NEW PUB.seq:*

3: /cgn2_6/ptcdata/2/pubpna/US06_NEW PUB.seq:*

4: /cgn2_6/ptcdata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptcdata/2/pubpna/US08_NEW PUB.seq:*

6: /cgn2_6/ptcdata/2/pubpna/US08_NEW PUB.seq:*

7: /cgn2_6/ptcdata/2/pubpna/US08_NEW PUB.seq:*

8: /cgn2_6/ptcdata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptcdata/2/pubpna/US09_PUBCOMB.seq:*

9: /cgn2_6/ptcdata/2/pubpna/US09_PUBCOMB.seq:*

10: /cgn2_6/ptcdata/2/pubpna/US09_PUBCOMB.seq:*

11: /cgn2_6/ptcdata/2/pubpna/US09_NEW PUB.seq:*

13: /cgn2_6/ptcdata/2/pubpna/US09_NEW PUB.seq:*

14: /cgn2_6/ptcdata/2/pubpna/US10B_PUBCOMB.seq:*

15: /cgn2_6/ptcdata/2/pubpna/US10B_PUBCOMB.seq:*

16: /cgn2_6/ptcdata/2/pubpna/US10B_PUBCOMB.seq:*

17: /cgn2_6/ptcdata/2/pubpna/US10B_PUBCOMB.seq:*

18: /cgn2_6/ptcdata/2/pubpna/US10B_PUBCOMB.seq:*

19: /cgn2_6/ptcdata/2/pubpna/US10B_PUBCOMB.seq:*

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19: /cgn2_6/ptcdata/2/pubpna/US10B_PUBCOMB.seq:*

20: /cgn2_6/ptcdata/2/pubpna/US10B_PUB.seq:*

20: /cgn2_6/ptcdata/2/pubpna/US10B_PUB.seq:*

20: /cgn2_6/ptcdata/2/pubpna/US10B_PUB.seq:*
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
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1385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MEAHALTIRLTNKVEFPFLV......DISKEVGEASIKVPQLKMEI 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:•
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.5
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2950.230 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	000	Result
44442	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	NO.
279.5 279.5 279.5 279.5 277.5 277.5 277.5 275.5	1385 1385 1385 1385 1385 1385 1385 1385	Score
19.00.00 19.00.00	1	Query
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Sequence 9682, Ap Sequence 9682, Ap Sequence 39301, A Sequence 1977, A Sequence 19220, A Sequence 25354, A Sequence 31809, A Sequence 6207, Ap Sequence 20511, A	177, App 23, App 23, App 23, App 23, App 23, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, App 21, A	Description

## ALIGNMENTS

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RESULT 1

US-10-120-988-177

Sequence 177, Application US/10120988

Publication No. US20030219745A1

GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Geodarich, Ryle
APPLICANT: Haug, Duraui
APPLICANT: Mang, Duraui
APPLICANT: Wang, Duraui
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20030219745A1el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 802CON
CURRENT APPLICATION NUMBER: US/10/120,988
CURRENT APPLICATION NUMBER: 09/774,528
PRIOR APPLICATION NUMBER: 09/774,528
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 441
SOFTWARE: pt_FL_genes Version 2.0
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Percent Similarity:
Best Local Similarity:
Query Match:
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ORGANISM: Homo sapiens
FEATURE:
NAME/KBY: CDS
LOCATION: (205)..(1305)
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LENGTH: 1416
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ProGlnLeuLysMetGluIle 267
                                      ProLysCysProLeuGlyValAspIleSerLysGluValGlyGluAlaSerIleLysVal
                                                                                                     IleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAspIleGluGlyIleArgTyrGlu
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; LENGTH: 1526
; TYPE: DNA
; ORGANISM: homo s
US-10-067-443-23
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Publication No. US20030082782A1

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
ITITLB OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED :
TITLB OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443

CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10

NUMBER OF SEQ 1D NOS: 71
SOPTWARE: PatentIn version 3.0
SEQ ID NO 23
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AlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThr
                                              CysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyVal
                                                                                                                      ThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeuPhe
                                                                                                                                                                                 GluLysGluGlyIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAla
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                                                                                                        ACAGTACAGCACAATGGCATGTCATCTTGTGAAAAGAACACATCGGGCTATTCTGTTT
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CURRENT APPLICATION NUMBER: US/10/649,273
CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR PILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR FILING DATE: 2002-04-10
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.2
SEQ ID NO 23
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Best Local Similarity:
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Publication No. US20040043407A1

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
FILE REFERENCE: D0073 CNT
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CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
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TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
FILE REFERENCE: D0073 DIV
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ORGANISM: homo
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Sequence 1, Application US/10067443

Publication No. US20030082782A1

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
ITITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A N
ITITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443

CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10

NUMBER OF SEQ ID NOS: 71
SOFTWARE: PAtentIn version 3.0

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 TYPE: DNA
ORGANISM: Homo
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CURRENT APPLICATION NUMBER: US/10/649,273
CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
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TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE,
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TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
FILE REFERENCE: D0073 DIV
CURRENT APPLICATION NUMBER: US/10/651,722
CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21, Applica Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.0 SEQ ID NO 21 LENGTH: 1387
                                                                                                                                                                                                                                                                                                          APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR PILING DATE: 2001-04-10
PRIOR PILING DATE: 2001-04-10
NUMBER: OF SEQ ID NOS: 71
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US-10-649-273-21
; Sequence 21, Application US/10649273
; Publication No. US20040043407A1
; GENERAL INFORMATION:
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 PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
                                                                              APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING
FILE REFERENCE: DO073 CUT
CURRENT APPLICATION NUMBER: US/10/649,273
CURRENT FILING DATE: 2003-08-27
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; PRIOR FILING DATE: 2001-04-10; NUMBER OF SEQ ID NOS: 71; SOFTWARE: PatentIn version 3.2; SEQ ID NO 21; LENGTH: 1387; TYPE: DNA; ORGANISM: homo sapiens
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GlyIleArgTyrGluProLysCysProLeuGlyValAspIleSerLysGluValGlyGlu
                                                                                                AlaThrGlnCysThrLeuLeuCysProProProArgLeuCysThrAspAsnGlyIleMet 215
                                                                                                                                                                                                                               ArgAlaIleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuVal 175
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Mismatches:
Indels:
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Sequence 21, Application US/10651722

Publication No. US20040048302A1

GENERAL INFORMATION:

APPLICANT: Briscol-Myers Squibb Company

FILE REFERENCE: D0073 DIV

CURRENT APPLICATION NUMBER: US/10/651,722

CURRENT APPLICATION NUMBER: US 60/266,518

PRIOR APPLICATION NUMBER: US 60/266,518

PRIOR FILING DATE: 2001-02-05

PRIOR APPLICATION NUMBER: US 10/067,443

PRIOR APPLICATION NUMBER: US 60/282,814

PRIOR APPLICATION NUMBER: US 60/282,814

PRIOR APPLICATION NUMBER: US 50/282,814

PRIOR FILING DATE: 2001-04-10

NUMBER OF SEQ ID NOS: 71

SOFTWARE: PatentIn version 3.2

SEQ ID NO 21

LENGTH: 1387

TYPE: DNA

ORGANISM: homo sapiens
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Best Local Similarity:
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Leiby, Kevin R.

APPLICANT: Kapeller-Libermann, Rosana

APPLICANT: Glucksmann, Maria A.

ITILE OF INVENTION: 38650, 28472, 5495, 65507, 81588, AND

ITILE OF INVENTION: 14354 METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND

ITILE OF INVENTION: THEREOF

FILE REFERENCE: 381552004900

CURRENT APPLICATION NUMBER: US/10/012,140

CURRENT FILING DATE: 2001-11-08

PRIOR APPLICATION NUMBER: 60/246,768

PRIOR APPLICATION NUMBER: 60/246,772

PRIOR FILING DATE: 2000-11-09

PRIOR APPLICATION NUMBER: 60/249,185

PRIOR FILING DATE: 2000-11-15

PRIOR FILING DATE: 2000-11-15

PRIOR FILING DATE: 2000-11-15

PRIOR FILING DATE: 2000-11-15

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                                                                                                                                                                                                                                                                                                 SEQ ID NO 6
                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                         LENGTH: 1245
TYPE: DNA
ORGANISM: Homo sapiens
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Conservative:
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APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Glucksmann, Maria A.
APPLICANT: Glucksmann, Maria A.
TITLE OF INVENTION: 38650, 28472, 5495, 65507, 81588, AND
TITLE OF INVENTION: 14354 METHODS AND COMPOSITIONS OF HUMAN PRO7
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 38155200490
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: 60/246,768
PRIOR APPLICATION NUMBER: 60/246,768
PRIOR APPLICATION NUMBER: 60/246,772
PRIOR FILING DATE: 2000-11-08
FRIOR APPLICATION NUMBER: 60/249,185
PRIOR APPLICATION NUMBER: 60/249,185
PRIOR APPLICATION NUMBER: 60/249,185
PRIOR FILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 49
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 1820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/10012140 Publication No. US20030009017A1 GENERAL INFORMATION:
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ORGANISM: Homo FEATURE:

sapiens

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; NAME/KEY: CDS
; LOCATION: (146)...(1390)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1820)
; OTHER INFORMATION: n = A,T,C or
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DB:
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                                                                                                      IleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAspIleGluGlyIleArgTyrGlu 240
                                                                                                                                                                                                                           AlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThr 200
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ProGlnLeuLysMetGluIle 267
                           ProLysCysProLeuGlyValAspIleSerLysGluValGlyGluAlaSerIleLysVal 260
                                                                                     ATTGAAAGACTACGTGCTTGGGCATTTTACATGACATAGAAGGCATCCGCTATGAA 1306
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 400
; LENGTH: 2208
; TYPE: DNA
; ORGANISM: Homo sapiens
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APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHIKO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOVUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NASUHO, YASUHIKO
TITLE OF INVENTION: NUMBER: US/10/094,749
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2001-09-14
PRIOR PRIOR DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
PRIOR PELING DATE: 2001-09-14
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APPLICANT: SUGIYAM
APPLICANT: OTSUKI,
APPLICANT: WAKAMANN
APPLICANT: SATO, H
APPLICANT: ISHII,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 400, Application US/10094749 Publication No. US20030219741A1 GENERAL INFORMATION:
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OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YURI
              LeuhleircGlmCl;/AsmArgFheHisFheAspIleirysFroProLeuHisHisAlairys 100
                                                                                                                                    LeuLeuGlyLysSerLeuAspIleAlaProGlyAspMetLeuAspLysValAlaArgArg
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AsnCysAspPheSerPheThrGlyLeuGlnHisValThrAspLysIleIleMetLysLys 120

ORGANISM: Homo sapiens   FEATURE:	CURREN CURREN CURREN PRIOR PRIOR PRIOR PRIOR PRIOR INMBER SOFTWA SEQ ID LENGT	US-10-723-860-7447 US-10-723-860-7447, Application US/10723860 ; Sequence 7447, Application US/10723860 ; Publication No. US20040253606A1 ; GENERAL INFORMATION:    APPLICANT: Aziz, Natasha    APPLICANT: Ginsburg, Wendy M.    APPLICANT: Ginsburg, Wendy M.    APPLICANT: Albert ; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma, Compositions & TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators	Oy 261 ProGlnLeuLysMetGluIle 267	Qy 241 ProLysCysProLeuGlyValAspIleSerLysGluValGlyGluAlaSerIleLysVal 260	Qy 221 IleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAspIleGluGlyIleArgTyrGlu 240 Db 1435 1435	Qy 201 LeuLeuCysProProProProArgLeuCysThrAspAsnGlyIleMetIleAlaTrpAsnGly 220	Qy 181 AlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThr 200	Qy 161 CysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyVal 180	Qy 141 ThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeuPhe 160 	Qy 121 GluLysGluGlyIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAla 140	
RESULT 15 US-10-067- Sequence Publicat GENERAL APPLICA TITLE 0 TITLE 0 TITLE RE CURRENT CURRENT CURRENT PRIOR A PRIOR A PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR B PRIOR	8 8 8 8	\$ \$ \$ \$ \$ \$	유 왕	Qy dd	g &	B 8	B 8	유 성	g <i>Q</i>	B 8	Db
SULT 15 -10-067-443-20 -10-067-443-20 -10-067-443-20 Sequence 20, Application US/10067443 Publication No. US20030082782A1 GENERAL INFORMATION: APPLICANT: Bristol-Myers Squibb Company TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED INTITLE OF INVENTION: SPINAL CORD, MP-1 FILE REFERENCE: DO073 NP CURRENT APPLICATION NUMBER: US/10/067,443 CURRENT FILING DATE: 2002-02-05 PRIOR APPLICATION NUMBER: US 60/266,518 PRIOR PILING DATE: 2001-04-10 PRIOR APPLICATION NUMBER: US 60/282,814 PRIOR PILING DATE: 2001-04-10 NUMBER OF SEQ ID NOS: 71 SOFTWARE: Patentin version 3.0 SEQ ID NO 20	241 ProLysCysProLeuGlyValAsplieSerLysGluValGlyGluAlaSerIleLysVal 260  241 ProLysCysProLeuGlyValAsplieSerLysGluValGlyGluAlaSerIleLysVal 260  260TGATGTCCTCTTGGAGTAGACATATCAAAAGAAGTTGGAGAAGCTTCCATAAAAGTA 2149  261 ProGlnLeuLysMetGluIle 267	AlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThr	161 CysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyVal 180 	141 ThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeuPhe 160 	121 GluLysGluGlyIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAla 140 	101 ABRCYBABPPheSerPheThrGlyLeuGlnHiBValThrAspLySIleIleMetLyBLyS 120 	81 LeuAlaLysGlnGlyAsnArgPheHisPheAspIleLysProProLeuHisHisAlaLys 100 	61 LeuSerLeuIleLysHisProGluCysSerThrMetSerGlyGlyLysAlaIleGluHis 80 	41 LeuLeuGlyLysSerLeuAspIleAlaProGlyAspMetLeuAspLysValAlaArgArg 60 	21 LeuLeuIleSerGlyGlyHisCysLeuLeuAlaLeuValGlnGlyValSerAspPheLeu 40 	

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RESULT 2
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O-sialoglycoprotein endopeptidase gcp [imported] - Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 18-Nov-2002

Agrobacterium tumefaciens (strain C58

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C;Accession: AB2902
R;Mood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, R;Mood, D.W.; Setubal, J.C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, Perage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, P; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Go
                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-366 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK88373.1; PID:g15157858; GSPDB:GN00169
C;Genetics:
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C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C;Accession: D97677
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A; Map position: cir
C; Superfamily: O-s:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Gold A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2323-2328, 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-365 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: circular chromosome C;Superfamily: O-sialoglycoprotein endopeptidase
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                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
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                                                                                                     Query Match
Best Local S
Matches 90
                                                                                                                                                                                                     Superfamily: O-sialoglycoprotein endopeptidase
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKFPLHHAKNCDFSFTGL----QHVTDKI
                                                    سر
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 24.4%; Score 338; DB 2; Length 365. Similarity 34.9%; Pred. No. 1.1e-22; 90; Conservative 40; Mismatches 98; Indels
                                                                                                                               Similarity
                          MEAHALTIRLINKVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VASGGVASNFYIRRALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDI 234
LEGHALTARLTDGLSFPYLMLLVSGGHTQLVLVRGVGEYERWGTTIDDALGEAFDKTAKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DALEVAPRSRWPLDGSAE 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APLSEQD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGL-PYP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGIRYEPKCPLGVDISKE 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VVAGGVAANQETRQTLQALCDTHGFRFVAPPHRLCTDNAAMTAWAGLERMAEG----RQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMKKEKEEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNA--VL
                                                                                                                                                                                                                                  circular chromosome
                                                                                                        Conservative
                                                                                                                          24.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----IADICASFOKAVSRTLKDRIGRGLARFKVE--FPHINGEPAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -GGPAVENAAKGDPDRFPLPRPMVGEARLDFSFSGLKTAVRQAATAI
                                                                                                     40; Mismatches
                                                                                                                          Score 338; DB 2; Length 366; Pred. No. 1.1e-22;
                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [imported] - Agrobacterium
                                                                                                  30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30;
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                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W
                                                                                                                     O-sialoglycoprotein endopeptidase (EC 3.4.24.57) [imported] - Brucella melicipspecies: Brucella melitensis
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
                                                                                                                                                                                                   RESULT 5
AB3274
                       C;Accession: AB3274
R;DelVecchio, V.G.; Kapatral, V.; Redkar,
R;DelVecchio, V.G.; Kapatral, V.; Redkar,
R;DelVecchio, V.G.; Kapatral, V.; Redkar,
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448
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The genome

sequence of the facultative intracellular pathogen Brucella melitensi atral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, N B.; Selkov, B.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesso U.S.A. 99, 443-448, 2002

Brucella melitensis

(strain

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A;Gene:
C;Superf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Andersson, S.G.E.; Zomorodipour, A.; Ande Nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia A;Reference number: A71630; MUID:99039499; A;Accession: E71711
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B71711
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A;Experimental source: strain Madrid E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: E71711
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable o-sialoglycoprotein endopeptidase (gcp) RP037 - Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-387 <AND>
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: O-sialoglycoprotein endopeptidase;
                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                   196
                                                                       278 LKSFRKDEFNWKPLECITRPKYRIHIQNSYRSNLLNDTIVIAGGVAANKYLQEILSDCTR 337
                                                                                                            164
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                                                                                                                                                                                                                                                                                                                                       1 MEAHALTIRLTNKVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARR
                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
87; Conserv
                                                                                                                                                                                                                             LNL-----SPPGGPEIEKRÄKLGNPHKYKFPKPIINSGNCNMSFSGLKTAVRTLIMNL 225
                                                                                                                                                                                                                                                                LSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DALEVAPRSRWPLDGSAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VASGGVASNYYIRRALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDI 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APLSEQD------IADICASFQKAVSRTLKDRIGRGLARFKVE--FPHINGEPAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMKKEKEEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNA--VL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGL----QHVTDKI
PYGYRLIAPPMHLCTDNAAMIAYAGLER
                                 ATQCTLLCPPPRLCTDNGIMIAWNGIER
                                                                                                                                              KEVNDSV-----INDIAASFOFTIGAILSSKMQDAIRLYKQILNDYYEDINHPTKLN 277
                                                                                                                                                                                 KEKEEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQ---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGIRYEPKCPLGVDISKE 252
                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                             24.4%; Score 338; DB 2;
32.5%; Pred. No. 1.1e-22;
tive 38; Mismatches 83
                                                                                                          -----LLPQN------NAVLVASGGVASNFYIRRALEILTN 195
                                   223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prowazekii and the origin of mitochondria PMID:9823893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          not shown; translation not
                                                                                                                                                                                                                                                                                                                                                                                 83;
                                                                                                                                                                                                                                                                                                                                                                                                                   Length 387;
                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                 60;
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A;Reference number: AD325
A;Accession: AB3274
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-359 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
E97707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.B.; Barbe, V.; Samson, Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: B97707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O-sialoglycoprotein endopeptidase (EC 3.4.24.57) [imported] - Rickettsia conorii c;Species: Rickettsia conorii C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001 C;Accession: E97707
                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: O-sialoglycoprotein endopeptidase C;Keywords: hydrolase; metalloproteinase
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C;Superfamily: O-sialoglycoprotein endopeptidase
C;Keywords: hydrolase; metalloproteinase
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A;Cross-references: GB:AE006914; PIDN:AAL02599.1; PID:g15619097; GSPDB:GN00173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE008917; PIDN:AAL51357.1; PID:g17982056; GSPDB:GN00190
                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 81
                                                                                                                                                                                                                                                                                                                                                                                                                Genetics:
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Best Local Similarity
 276
                                   179
                                                                    226
                                                                                                       120
                                                                                                                                          173
                                                                                                                                                                                                                113
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                                                                                                                                                                                                                                                                                      81;
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                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                          INL----AFPGGPEIEKRAKLGDPHKYKFPKPIINSGNCNMSFSGLKTAVRTLIMTL 225
                                                                                                                                                                                                              VASGGVASNFYIRRALBILTNATQCTLLCPPPRLCTDNGIMIAWNGIER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGL-----QHVTDK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMK- 119
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 GVAANKYLOKILSSCAKTYGYRLIYPPIHLCTDNAAMIAYAGLER 320
                                 GVASNFYIRRALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIER 223
                                                                    KBINDTV-----INDIAASFQFTIGEILSSKVQDAIRAYEQITNNFDKKN--IVIAG
                                                                                                     KEKEEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQ-RDLLPQNNAVLVASG 178
                                                                                                                                                                                                                                                MEAHALTIRLTNKVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VVAGGVAANKTLRAALENLCTRHGFAFIAPPLNLCTDNAAMIAWAGAER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                    23.8%; Score 329.5; DB 2; ilarity 36.0%; Pred. No. 5.8e-22; Conservative 40; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AD3252; PMID:11756688
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37.6%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 334.5; DB 2;
Pred. No. 2.2e-22;
33; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83; Indels
                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                        Length 344;
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R;Stover, C.K.; Pham, X.Q.; Brwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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A;Title: Complete Genome Sequence of Caulobacter crescentus.
                                                                                                             A; Gene: gcp; P/C; Superfamily:
                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-341 <STO>
A;Cross-references: GB:AE004494; GB:AE004091; NID:g9946446; PIDN:AAG03969.1;
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Accession: H83572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O-sialoglycoprotein endopeptidase PA0580 [imported] - Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa . C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: H83572
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C;Superfamily: O-sialoglycoprotein endopeptidase
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A;Accession: F87257
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C;Species: Caulobacter crescentus
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Query Match 21.0%; Score 291.5; DB 2
Best Local Similarity 35.4%; Pred. No. 1.5e-18;
Matches 87; Conservative 37; Mismatches 99
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36.3%; Pred. No. 1.2e-21;
htive 36; Mismatches 99
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K.; Lim,
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O-sialoglycoprotein endopeptidase (EC 3.4.24.57) - N;Alternate names: sialoglycoproteinase C;Species: Haemophilus influenzae
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: G70369
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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C;Spectes: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: G70369
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A; Residues: 1-335 < AQF>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KKEKNVRK-----EDIAYSFQETVVEILLEKS----LWAMKKTGIKR----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.0%; Score 290.5; DB 2; ilarity 34.3%; Pred. No. 1.8e-18; Conservative 46; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
                                                                 Haemophilus influenzae (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 35;
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A;Accession: H64074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: H64074
C;Accession: H64074
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, R;Fleischmann, R.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, Goayne, J.D.; Scott, J.; Shirley, R.C.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M., D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M., D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M., D.M.; Brandon, R.C.; Venter Science 269, 496-512, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Genome sequence of Yersinia pestis, the causative A;Reference number: AB0001; MUID:21470413; PMID:11586360 A;Accession: AI0079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: AI0079
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre
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                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: gcp
C;Superfamily: O-sialoglycoprotein endopeptidase
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A; Residues: 1-337 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable glycoproteinase gcp [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
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                     KEKEEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNN-AVLVASG 178
                                                                                                                                             RLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMK 119
                                                                                                                                                                                                          MEGHLLAPMLEENAPEFPFVALLVSGGHTQLISVTGIGEYLLLGESVDDAAGEAFDKTAK 171
                                                                                                                                                                                                                                      MEAHALTIRL-TUKVEFPFLYLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVAR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGVSANKKLRETLAHLMQNLGGEVFYPQPQFCTDNGAMIAYTGFLRLKQG 321
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                                                                                         -GGPMLSRMAQQGTVGRFTFPRPMTDRPGLDFSFSGLKTFAANTIRA 224
                                                                                                                                                                                                                                                                                                                               35; Mismatches 102;
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Barrell,
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probable O-sialoglycoprotein endopeptidase [imported] - Escherichia coli (strain C;Species: Escherichia coli (c;Species: Escherichia coli (c;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 C;Datesion: C91122 C;Accession: C91122 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Hagaswara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S:, Moule, S:, O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C:, Quail, M:, Rutherford, K:, Simmonds, M.; A;Title: Complete genome sequence of a multiple drug resistant: A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AG0892
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-337 <PAR>
                 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and A;Rcfercace number: A39629; MUID:21156231; PMID:11258796 A;Accession: C91122 A;Status: preliminary
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A;Gene: STY3387
C;Superfamily: O-sialoglycoprotein endopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable glycoprotease [imported] - Salmonella enterica subsp. enterica serovar (Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AG0892
A; Molecule type:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 20.2%; Score 279.5; DB 2; Similarity 32.9%; Pred. No. 1.8e-17; 81; Conservative 35; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                             VASNFYIRRALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDIEGIRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEGHLLAPMLEDNPPDFPFVALLVSGGHTQLISVTGIGQYELLGESIDDAAGEAFDKTAK 171
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probable O-sialoglycoprotein endopeptidase ygjD [imported] - Escherichia coli C;Species: Escherichia coli C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: B85967
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE005174; NID:g12517643; PIDN:AAG58198.1; GSPDB:GN00145; UWGP:Z44JA;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Genome sequence of enterohemorrhagic Escherichia A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: B85967
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C;Superfamily: O-sialoglycoprotein endopeptidase
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Superfamily:
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VASNFYIRRALBILTNATQCTLLCPPPRLCTDNGIMIAWNGIBRLRAGLGILHDIBGIRY 239
                                                                                                                                                                                                                                                                                                                                          RLSLIKHPECSTMSGGKAIEHLAKQGNRFHPDIKPPLHHAKNCDPSFTGLQHVTDKIIMK 119
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                                                                                                                                    --RDNGTDD----QTRADIARAFEDAVVDTLMIKCKRAL-----DLTGFKR--LVMAGG
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33.3%; Pred. No. 2.2
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Pred. No. 2.2e-17;
36; Mismatches 101;
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K.; Ap
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hypothetical protein C01G10.10 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000 C;Accession: T18825 R;Matthews, L.
Search completed: February 16, 2005, 13:09:22 Job time: 14.1891 secs
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A;Map position: 5

A;Introns: 31/2; 72/3; 122/2; 177/1; 272/3; 315/1; 353/2
C;Superfamily: O-sialoglycoprotein endopeptidase
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A;Residues: 1-421 <WIL>
A;Cross-references: EMBL:Z81030; PIDN:CAB02716.1; GSPDB:GN00023; CESP:C01G10.10
A;Experimental source: clone C01G10
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A;Reference number: Z19027
A;Accession: T18825
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Command line parameters:

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## ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL RESULT 1 BQ423651 LOCUS COMMENT **FEATURES** DEFINITION 8077708 1 (bases 1 to 870) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. BQ423651 870. AGENCOURT 7790948 NIH\_MGC\_72 5', mRNA Bequence. BQ423651 BQ423651.1 GI:21118966 High quality sequence stop: 'Location/Qualifiers CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution informati found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAMI3342 row: 1 column: 21 Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC/DCTD/DTP Homo sapiens (human) /mol\_type="mRNA" /db\_xref="taxon:9606" organism="Homo sapiens" clone="IMAGE:6065828" bp mRNA lineal Dec 20.2. Homo sapiens cDNA clone IMAGE:6065828 Consortium (LLNL) linear information can EST 23-MAY-2002 þ

829596 MA

Query DB:

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/lab host="DH10B (phage-resistant)"
/clone_lib="NIH MCC_72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
/site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life Technologies."
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                                                                                                                                                                                                          Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                     Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (S-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Group Phase I & II Team.
Analysis of the mouse transcriptome based of 60,770 full-length cDNAs
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Functional annotation of a full-length mouse
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mus musculus (house mouse)
cDNA library was prepared and sequenced in Mouse Genome 
Encyclopedia Project of Genome Exploration Research Group
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6 (bases 1 to 2284)
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Please visit our web site for further details.
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URL:http://fantom.gsc.riken.jp/.
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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AKO11265

MIS musculus 10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2610001M19 product:similar to PUTATIVE SIALOGLYCOPROTEASE TYPE 2 [Homo sapiens], full insert sequence.
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Ni Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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6 (bases 1 to 1622)
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/protein_id="Bab27506.1"
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/db_xref="GI:12847276"
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similar to PUTATIVE SIALOGLYCOPROTEASE TYPE 2 [Homo
sapiens] (SPTR|Q9H4B0, evidence: FASTY, 80%ID, 100%length,
                                                                                                                                                                                                                                                                                                                      /tissue type="whole body"
/clone_Tib="RIKEN full-length enriched mouse
/dev_stage="10 days embryo"
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/strain="C57BL/6J"
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1 (bases 1 to 640)

Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A.,
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.

Expressed sequence tag analysis of human retina for the NEIBank
Project: Retbindin, an abundant, novel retinal cDNA and alternative splicing of other retina-preferred gene transcripts

Mol. Vis. 8 (4), 196-204 (2002)
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Plate: 03 row: d column: 11
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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hd03d11.y1 Human Retina
Homo sapiens cDNA clone
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Fax: 301 496 0078
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Section on Molecular Structure and Function
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                         GluHisLeuAlaLysGlnGlyAsnArgPheHisPheAspIleLysProProLeuHisHis 98
                                                                                                              ArgArgLeuSerLeuIleLy8Hi8ProGluCy8SerThrMetSerGlyGlyLy8AlaIle
  GAACATTTGGCCAAACAAGGAAATAGATTTCATTTTGACATCAAACCTCCCTTGCATCAT 122
                                                                                       AGAAGACTTTCTTTAATAAAACATCCAGAGTGCTCCACCATGAGTGGTGGGAAAGCCATA
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/note="Organ: Sye; Vector: pspORT1; Neural retina tissue /note="Organ: Sye; Vector: pspORT1; Neural retina tissue was dissected from two 80 year old donors with no observed eye disease. 100ug of total RNA was used for library construction. A directionally cloned cDNA library in the pspORT1 vector (Life Technologies) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's Instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I
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was performed on the unamplified library at the NIH
Intramural Sequencing Center (NISC)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                primer-adapter
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/lab_host="EMDH10B"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="hd03d11"
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Matches:
Conservative:
Mismatches:
Indels:
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REFERENCE
AUTHORS
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                                                                                                        E 1 (bases 1 to 852)

E 1., W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On May 13, 2003 this sequence version replaced gi:30611736.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-0ligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a
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BX391919
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EST.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                 For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOBAIO35ZEO7_CSO3317_1&c=1240.r
                                                                                          division of Invitrogen. This sequence
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Location/Qualifiers
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/organism="Homo sapiens"
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/clone="CSODK001YE02"

ORIGIN

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RESULT 6
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SOURCE
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                                                                                     Mus musculus O-sialoglycoprotein clone IMAGE:1226118), containing
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                                                                                                                                                                                                                               LeuLeuCysProProProArgLeu 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTTTGATTTCTGGAGGTCACTGTCTGTTGGCATTAGTTCAAGGAGTTTCAGATTTTCTG
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                musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cell_type="HELA CELLS COT 25-NORMALIZED"
/cell_line="HELA"
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                                                    GI:21040459
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Matches:
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
US-10-649-273-2_COPY_148_414 (1-267)
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TITLE
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Glbbs, R.A.,

Fahey, J., Helton, B., Ketteman, M., Wadan, A., Touchman, J. W., Green, B.D.,

Fahey, J., Helton, B., Ketteman, M., Wadan, A., Creen, B.D.,

Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schmerch, A., Schein, J.B., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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COntact: MGC help deek
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Marcello Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
DNA Sequencing by: Institute for Systems Biology
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21312463
This clone has the following problem: frame shifted.

Location/Qualifiers
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Submitted (20-MAY-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Strausberg, R.
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/clone_tib="soares_thymus_2NbMT"
/lab_host="DH10B"
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           x BC030671 (1-1609)
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Matches:
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AUTHORS
TITLE
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ORGANISM
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                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 701)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                          BE740611.1 GI:10154603
EST.
     Unpublished (1999)
                                                                                                                                                                                Homo sapiens (human)
                                                                                                                                                                                                                                                                                mRNA sequence.
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Tissue Procurement: DCTD/DTP
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heCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyV
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                                                                        laThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeuP
                                                                                                                                                                                GGAAACAAGAGGAAGGTATTGAGAAGGGGCAAATCCTGTCTTCAGCAGCAGACATTGCTG
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TITLE
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Tissue Procurement: DCTD/DTP/Gazdar

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2603 row: d column: 15

High quality sequence stop: 584.

Location/Qualifiers

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Contact: Robert Strausberg, Ph.D.
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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AGENCOURT_8863711 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6423902
5', mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                          MetGluAlaHisAlaLeuThrIleArgLeuThrAsnLysValGluPheProPheLeuVal
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 CTTTTGATTTCTGGAGGTCACTGTCTGTTGGCATTAGTTCAAGGAGTTTCAGATTTTCTG
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/clome lib="NIH_MGC_18"
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/db_xref="taxon:9606"
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829596 MARC:
CF362328
CF362328.1 (
                                                                                                                                                                                                                                                                                                              1 (bases 1 to 658)
Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Fox, J.,
Wise, T.A., Nonneman, D.J., Wray, J.E. and Keele, J.W.
A second set of porcine ESTs from a pooled-tissue normalize
                                                                         Seq
                                                                                       Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified cross_match v0.990329.

Plate: SRG8015 row: H column: 12
                                                                                                                                                                                                                                                         Contact: Smith
                                                                                                                                                                                                                                                                            Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa (pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST.
                                                                                                                                                                                                                     USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166,
                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                   Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                  Bmail: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                 library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----AsnGlyIleGluArg---LeuArgAlaGlyLeuGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sGluLysGluGlyGleGluLysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAl
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                                                                         primer: TAGAAGGCACAGTCGAGG.
/organism="Sus scrofa"
/mol_type="mRNA"
                                                      Location/Qualifiers
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3PIG Sus scrofa cDNA 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GI:34161882
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Cetartiodactyla; Suina; Suidae;
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0166, USA
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, mRNA sequence.
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Euteleostomi; Sus.

with

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Gallus gallus (chicken)
Gailus gallus
Gailus gallus
Chordata; Chordata; C
Archosauria; Aves; Neognathae;
                                                                     sequence.
CF257246
CF257246.1
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  Phasianinae; Gallus.
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                                                                                                                                                                 ACTCTGTTGTGTCCTCCCCAGACTATGCACTGATAATGGCATTATGATTGCATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="PH108"
/clone_lib="MARC 3PIG"
/note="Vector: pcDNA3.1, Site_1: EcoRI; Site_2: NotI;
Library made with RNA pooled from multiple tIssues
including brain, liver, muscle, placenta/endometrium,
ovary, testes, and bone marrow."
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            Craniata; Veri; Galliformes;
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                        Vertebrata;
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             Phasianidae;
                         Euteleostomi;
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Wittzell,H., Bed'Hom,B., Morin,V., Yc
Chausse,A.M. and Zoorob,R.
A collection of chicken ESTs from act
Unpublished (2003)
Contact: Zoorob R
UPR 1983
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Tel: 33 1 49 58 35 00
Fax: 33 1 49 58 33 81
Email: zoorob@vjf.onrs.fr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNRS
                                                                                                                                                                                                                                                                                                         LeuLeuGlyLysSerLeuAspIleAlaProGlyAspMetLeuAspLysValAlaAargArg
LeuLeuCysProProProArgLeuCysThrAspAsnGlyIleMetIleAlaTrpAsnGly
                         AlaSorAonThoTyrIleArgAlaLeuGlüileLeuThrAsnAlaThrGinCysThr
                                                                  TGCATGAAAAACAGCATATTATTACCAAAAACTGCAACTCTGGTTGTATCAGGAGGAGTT
                                                                                CysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyVal
                                                                                                                   GluLysGluGluGlyIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAla
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                                                                                                                                                                 GAAAAAGAAGGTATTCAAGAAGGGGAAATCCTGTCCTGCGTTAAGGACATCGCTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db xref="taxon:9031"
/ceI1_type="Splenocytes"
/clone_lib="PHA-activated
/note="Vector: pTriplEX2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Gallus
/mol_type="mRNA"
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CK941819
CK941819.1
EST.
Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                      Single pass sequencing. Bases called and trimmed with phred 0.000925 using options -trim alt " -trim fasta. Vector identified by cross match using options -minmatch 12 -minscore 18 Plate: 12 row: F column: 24 Seq primer: AGCGGATAACAATTTCACACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 637)
Sonstegard, T.S., Van Tassell, C.P., Matukumalli, L.K., Harhay,
G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.
Production of EST from cDNA libraries derived from immunologically
activated boyine gut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2004)
Contact: Tad S. Sonstegard
Contact: Tad S. Sonstegard
Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute
Badlg. 200 Rm2A BARC-East, Beltsville, N
                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 637.
Location/Qualifiers
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Mammalia; Eutheria;
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4065407 BARC 10BOV Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: tads@anri.barc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: 3015048414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovinae; Bos.
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                                                                                                                         /note=Torgan: Small Intestine; Vector: pAgen-1; Site 1: EcoRV; Site 2: NotI; Equimolar amounts of mRNA extracted from proximal jejunums of 18 and 21 wk old steers, and distal lleums of 14 day old calves. proximal jejunum exposed to C. oncophora for 3 and 6 weeks, and distal ileum exposed to C. parvum for 7 days"
                                                                                                                                                                                                                       /dev stage="Multiple"
/lab_host="DH10B T1 phage resistant"
/clone_lib="BARC 10BOV"
                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9913"
/clone="10BOV12_F24"
                                                                                                                                                                                                                                                                                             /sex="Male"
                                                                                                                                                                                                                                                                                                                                          strain="Holstein"
                                                                                                                                                                                                                                                                            tissue_type="Pooled"
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Email: est@watson.wustl.edu
Library constructed and donated by Foundation for Biomedical Research,
                                                                                                                                                                             McCarrey, J., Eddy, M., Marra, M., Hillier, L., Clifton, S., Martin, J., Wylie, T., Dante, M., Bowers, Y., Theising, B., Ritter, B., Tsagareishvili, R., Ronko, I., Maguire, L., Ken Bennett, J., Waterston, R. and Wilson, R.
                                                  Tel: 314 286 1800
Fax: 314 286 1810
                                                                                4444 Forest Park Parkway,
                                                                                                                                Contact: McCarrey/Eddy NIEHS Mouse
                                                                                                                                                 Unpublished (2002)
                                                                                                                                                                NIEHS Mouse
                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                          musculus (house mouse)
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   by J. McCarrey, Ph.D.
rch, Dept. of Genetics)
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241 213 221 273 201 333 393 161 453 513 121

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Best Local Similarity:
Query Match:
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Institute of
MGI:2069710
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                           LeuLeuGlyLysSerLeuAspIleAlaProGlyAspMetLeuAspLysValAlaArgArg
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Fax: 01612360409
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Department of Biomolecular Sciences
University of Manchester Institute
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                                                                                                                                                                                                       /clone_lib="CSEQCHN59" /clone_libs="CSEQCHN59" /clone_Torgan: limbs; Vector: pBluescript II KS(+); Site_1: /note="Torgan: limbs; Vector: pBluescript II KS(+); Site_1: /note="Torgan: limbs; Vector: pBluescript II KS(+); Site_1: /note="Torgan: limbs; Vector: promain | formalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Pollowing this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."
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/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
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 Caprinae; Ovis.
1 (bases 1 to 730)
Gossner,A. and Hopkins,J.
Ovine spleen\brain cDNA library
Unpublished (2004)
Contact: J Hopkins
                                                                          Ovis aries
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                EST.
Ovis aries (sheep)
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GTAGTGGCTGCTCATATTATCCAGCGGACACACCGAGCCATGCTCTTCTGCATGAAAAAC
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AV602901 Bos taurus kidd
3', mRNA sequence.
AV602901
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EST.
Bos taurus (cow)
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University of Edinburgh
Summerhall Square, Edinburgh, EH
Email: j.hopkins@ed.ac.uk
Plate: 04 row: N column: 08
Seq primer: Ml3reverse
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High quality sequence stop: Location/Qualifiers
                                                                                                                              CysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGly 179
                                                                                                                                                                                   GCAGTCCAGCACACCGTAGCCTGCCACGTTGCNAAAAGAACACATCGCGCTATTCTGTTC
                                                                                                                                                                                                     ThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeuPhe
                                                                                                                                                                                                                                     GluLysGluGluGlyIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAla 140
                                                                                                                                                                                                                                                                                                     AsnCysAspPheSerPheThrGlyLeuGlnHisValThrAspLysIleIleMetLysLys
                                                                                                                                                                                                                                                                                                                                                        LeuAlaLysGlnGlyAsnArgPheHisPheAspIleLysProProLeuHisHisAlaLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuLeuGlyLysSerLeuAspIleAlaProGlyAspMetLeuAspLysValAlaArgArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuLeuIleSerGlyGlyHisCysLeuLeuAlaLeuValGlnGlyValSerAspPheLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGGAGGCTCATGCACTTACTATTAGGTTAACAAATAAGGTAGAATTTCCATTTTTAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MetGluAlaHisAlaLeuThrIleArgLeuThrAsnLysValGluPheProPheLeuVal
                                                                                                                                                                                                                                                                                         AATTGTGATATTTTCTTTTTCTGGACTTCAACATGTTATTGATAAGATGATAATGCAGAAG
                                                                                                                                                                                                                                                                                                                                                                                              CTTTGCTTAATAAAACATCCAGAGTGCTCCACCATGAGTGGCGGGAAGGCTATAGAACAT
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                                                                545 bp
Bos taurus kidney fetus
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/clone_lib="Sheep_spleen\brain
/note="Vector: pSport1"
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/mol_type="mRNA"
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Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fuk
Tel: 81-248-25-5725
Fax: 81-248-25-5725
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Bitablishment of a high throughput EST sequencing system using poly(A) tail-removed cDNA libraries and determination of 36,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: kazusugi@cocoa.ocn.ne.jp
Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                        GASPLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyValAlaSerAsnPh 184
                                                                                                                                                                                                                                                                                              eSerPheThrGlyLeuGlnHisValThrAspLy8IleIleMetLy8Ly8GluLy8GluLy8GluG 124
oProProArgLeuCysThrAspAsnGlyIleMetIleAlaTrpAsnGlyIleGluArgLe 224
                                                                                                                                                                             CACCGTGGCCTGCCACATTGCAAAAAGAACACATCGTGCTCTTCTGCTTCTGCAAGCAGAG
                                                                                                                                                                                                   sThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnAr 164
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/note="Vector: pZL1; Site_1: Sal1; Site_2: Not1; Poly A
was deleted from a Not1 site"
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/dev_stage="fetus"
/lab_host="DH10B"
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/db_xref="taxon:9913"
/clone="E1KI013A07"
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                                                                                              ACGTGCTGGCTTGGGCATTTTTACACAACACAGAAGGCATCCGCTACGAACCAAAATGTCC
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                                            TCTTGGAGTAGATATATCAAAAGAAGTTGGAGAAGCTGCTATAAAAGTGCCAAGATTAAA
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Search completed: February 16, 2005, 21:04:47 Job time: 3184.37 secs

Copyright

GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.

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Result
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EMBL; AJ29148; CAC14666.1; -..

Genew; HGNC:23075; OSGEPL1.

GO; GO:0008450; F:O-sialoglycoprotein endopeptidase activity; IEA.

GO; GO:000823; F:peptidase activity; IEA.

GO; GO:0008270; F:zinc ion binding; IEA.

GO; GO:0008270; F:proteolysis and peptidolysis; IEA.

InterPro; IPR000905; Peptidase M22.

InterPro; IPR009180; Peptidase M22.

Pfam; PF00814; Peptidase M22; T...

Pfam; PF00814; Peptidase M22; T...
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SEQUENCE
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PIRSF; PIRSF004537; Osialglc_pptds; 1.
PRINTS; PR00789; OSIALOPTASE.
ProDom; PD002367; Peptidase_M22; 1.
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Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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0; Mismatches 1;
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RP SEQUENCE FROM N.A.

RC STRAIN=CZECH II; TISSUE=Mammary tumor;

RC STRAIN=CZECH II; TISSUE=Mammary tumor;

RX MEDLINE=22388257; PubMede12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE=22388257; PubMede12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE=22388257; PubMede12477932; DOI=10.1073/pnas.242603899;

RX Strausherg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heigh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heigh F.L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Wolley R.C., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,

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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RT "Generation and initial analysis of more than 15 000 6.11 locate temporal temporal for the form of the field of the form of the field of the form of the field of the form of the field of the form of the field of the form of the field of the form of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of the field of
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                                                                                                                  Query Match
Best Local Sim
Matches 233;
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Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; BC058172; AAH58172.1; -

GO; GO:0008450; F:O-sialoglycoprotein endopeptidase acti

GO; GO:0008270; F:zinc ion binding; IEA.

GO; GO:0008270; F:zinc endopeptidolysis; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

InterPro; IPR009180; Peptidase M22;

InterPro; IPR009180; Peptidase M22;

InterPro; IPR009180; Peptidase M22;

PFam; PF00814; Peptidase M22;

PIRSF; PIRSF004537; Osialglc_pptds; 1.
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                                                                                                                                                                                                                                                              PRINTS; PR00789; OSIALOPTĀSE. ProDom; PD002367; Peptidase M22; TIGRFAMs; TIGR00329; gcp; 1. Hypothetical protein. SEQUENCE 414 AA; 44962 MW; 0.
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Mus musculus (Mouse).
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.";
proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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87.3%; Pred. No. 4.60
Live 15; Mismatches
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SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Corpora quadrigemina;
STRAIN=CS7BL/6J; TISSUE=Corpora quadrigemina;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE X, Itch H., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Shibata K., Itch H., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Shibata K., Itch H., Itch M.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itch M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Kashiwagi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUB=Corpora quadrigemina;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                            SEQUENCE FROM N.A.

STRAIN-C57BL/6J; TISSUB-Corpora quadrigemina;

STRAIN-C57BL/6J; TISSUB-Corpora quadrigemina;

MEDLINE-20499374; PubMed=11042159; DOI=10.1101/gr.145100;

Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K.,

Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

"Normalization and subtraction of cap-trapper-selected cDNAs

prepare full-length cDNA libraries for rapid discovery of new

Genome Res. 10:1617-1630(2000).
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length
enriched library, clone:B230219017 product:similar to PUTATIVE
SIALOGLYCOPROTEASE TYPE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=C57BL/6J; TISSUE=Corpora The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                              the RIKEN Genome Exploration Research "Analysis of the mouse transcriptome 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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Mammalia; Eutheria;
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               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Lost sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last amoutation update)
Mus musculus 10 days embryo whole body cDNA, RIKEN
enriched library, clone:2610001M19 product:similar
SIALOGLYCOPROTEASE TYPE 2.
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RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/60; TISSUE=Corpora quadrigemina;

RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carminci P.,

RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carminci P.,

RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

RA Hori F., Imotani K., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

RA Tagawa A., Tokahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,

RA Tagawa A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

REMBI, AKO45669; BAC32450.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0008450; F:O-sialoglycoprotein endopeptidas
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0008270; F:zinc ion binding; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IE
InterPro; IPR000905; Peptidase M22.
InterPro; IPR009180; Peptidase M22.
InterPro; IPR009180; Pept M22 Ōsialgl.
Pfam; PF00814; Peptidase M22; 1.
PFRSP; PIRSF004537; Osialglc_pptds; 1.
PRINTS; PR00799; OSIALOPTASE.
PRODOM; PD002367; Peptidase M22; 1.
PIGRPAMS; TIGR00329; gcp; 1.
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Best Local
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SEQUENCE
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388
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  PKCPLGVDISREVAEAAI KVPRLKMAL
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Pred. No. 1.8e
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PRELIMINARY;

PRT;

414

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full-length to PUTATIVE

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STRAIN=C57BL/J; TISSUE=Whole body;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Aizawa K., Nagaka S., Sasaki N., Carninci P.,

KOnno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,

"RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";

Genome Res. 10:1757-1771(2000)
                                                                                                                                                                                                                                                      STRAIN=C57BL/6J; TISSUE=Whole body;
Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.,
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
MEROPS; M22.004; -. MGD; MCI:1919335; OBgep11.

GO; GO:0008450; F:O-sialoglycoprotein er GO; GO:0008233; F:peptidase activity; IE GO; GO:0008270; F:zinc ion binding; IEA.

GO; GO:0008270; P:proteolysis and peptid
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STRAIN-C57BL/6J; TISSUE=Whole body;

MEDLINE-20499374; PubMed=11042159; DOI=10.1101/gr.145100;

MEDLINE-20499374; PubMed=11042159; DOI=10.1101/gr.145100;
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STRAIN-C57BL/6J; TISSUE-Whole body;
MEDLINE-99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
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STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                  IEA
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EX. PhDMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Rax S.I., Wang J., Hrange C.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bobak S.A., McSewan P.J., McKernan K.J., Maiek J.A., Gunaratne P.H.,

RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Kraywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Alter S., T. Marra M.A.,

RA Alter S., Schnerch A., Schein J.E.,

RA Alter S., Schnerch A., Schein J.E.,

RA Alter S., Schnerch A., Schein J.E.,

RA Alter S., Schnerch A., Schein J.E.,

RA Alter S., Schnerch A., Schein J.E.,

RA Alter S., Schnerch A., Schein J.E.,

RA Alter S., Schnerch A., Schein J.E.,

RA Alter S., Schnerch A., Schein J.E.,

RA Alter S., Schnerch A., Schein J.E.,

RA Alter S., Schnerch A., Schein J.E.,

RA Alter S., Schnerch A., Schein J.E.,

RA Alter S., Schnerch A., Schein J.E.,

RA Alter S., Schnerch A., Schein J.E.,

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Best Local S
Matches 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-OCT-2004 (TrEMBLrel.
25-OCT-2004 (TrEMBLrel.
25-OCT-2004 (TrEMBLrel.
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25-OCT-2004
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                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical
                                                                                                                                                                             Jones S.J., Marra M.A.;
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                                                                                                                                                Generation and initial analysis
                                                                                                                   mouse
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ad. Sci. U.S.A.
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29; gcp; 1.
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Pred. No. 8.9e
L4; Mismatches
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Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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Scheetz T.E.,
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Matches 214
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X PubMed=14702039; DOI=10.1038/ng1285;
X Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
X Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
X Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
X Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
X Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
X Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
X Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawata M.,
X Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawata M.,
X A Sudo H., Kamihara K., Yakoi T., Furuya T., Kikkawa E., Omura Y.,
X A Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
X Ala Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
X Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
X Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
X Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
X Tangiya S., Komai P., Hara R., Takeuchi K., Arita M., Imose N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; BC078974; AAH78974.1; -...

GO; GO:0008450; F:O-sialoglycoprotein endopeptidase act GO; GO:0008270; F:zinc ion binding; IEA. GO; GO:0008288; P:proteclysis and peptidolysis; IEA. InterPro; IPR000905; Peptidase M22; InterPro; IPR009180; Pept M22 Goialgl. InterPro; IPR009180; Peptidase M22; 1. RP00914; Peptidase M22; 1. PIRSF: PIRSF004337; Osialglc_pptds; 1. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE. RPINTS; PR00789; OSIALOPTASE RPINTS; PR00789; OSIALOPTASE RPINTS; PR00789; OSIALOPTASE RPINT
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Q96NH5;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation updat
Hypothetical protein FLJ30879.
Homo sapiens (Human).
Chardata: Craniata; Vertebrat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
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Submitted (AUG-2004)
                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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Pred. No. 3.8e-87;
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R MEROPS; M22.004; ...

R GO; GO:0008450; F:O-sialoglycoprotein endopeptidase activity; IEA.

R GO; GO:0008233; F:peptidase activity; IEA.

R GO; GO:0008270; F:zinc ion binding; IEA.

DR GO; GO:0008270; F:zinc ion binding; IEA.

DR InterPro; IPR000905; Peptidase M22.

DR InterPro; IPR000905; Peptidase M22.

DR Pfam; PF000144; Peptidase M22; 1.

DR PIRSF; PIRSF004537; Osialglc_pptds; 1.

DR PRINTS; PR00789; OSIALOPTASE.

DR PRINTS; PR00789; OSIALOPTASE.

DR PRINTS; PR00789; OSIALOPTASE.

DR TIGRFAMS; TIGR00329; gcp; 1.
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RA Yoshikawa Y., Matsunawa H., Ichihara T., Shichata N., Sano S.,

RA Moriya S., Momiyama H., Satch N., Takami S., Terashima Y., Szuki O.,

RA Makagawa S., Sench A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,

RA Hishigaki H., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,

RA Yamazaki M., Watanabe K., Kumagai A., Takemoto M., Kawakami B.,

RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Pujiwara T.,

RA Cho T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,

RA Cho T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,

RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,

RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Camada M., Harai T., Noguchi S., Itoh T., Shigeta K., Senba T.,

RA Kawabata R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,

RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,

RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,

RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,

RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;

T. "Complete sequencing and characterization of 21,243 full-length human

T. COMBR.":
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Best Local
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                                                                                                                                                                         QBJFW3 PRELIMINARY; PRT; 404 AA.
QBJFW3; (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
S1:dZ21/013.4 (Novel glycoprotease).
Name=dZ72B14.6;
Babbage A.;
Submitted (SEP-2003) to
                                                                                                            Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniform
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                                        SEQUENCE PROM N.A.
                                                                            Cyprinidae; Dani
NCBI_TaxID=7955;
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EMBL; AK055441; BAB70923.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 79.8%; Score 1105; DB 2; Similarity 98.6%; Pred. No. 2.5e-86; 14; Conservative 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      364 AA;
                                                                                                Danio.
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  the EMBL/GenBank/DDBJ databases
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Best Local Similarity
Matches 165; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                Name-SI:d272B14.6;
Name-SI:d272B14.6;
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Paniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QBJFR7;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation updat
SI:dZ72B14.6 (Novel glycoprotease).
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                             Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. Clark G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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Best Local (
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Best Local (
                                                                                                                                                                             Matches 106;
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01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                       PRINTS; PR00789; OSIALOPTASE.

ProDom; PD002367; Peptidase M22; 1.

TIGRFAMs; TIGR00329; gcp; 1.

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SEQUENCE 401 AA; 43849 MW; CC94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-i- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AgCP14990 (Fragment).
Name-agCG46164; ORFNames=ENSANGG00000007922;
Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-PEST;
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                                                                                                             MQAHALMARMISTIPYPFLCLLVSGGHSLLVFVESTARFRLLGETLDDAPGEALDKIARR
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LKLRNVAKYAOMSGGQAİBAAAQQAGAKDTSAYBFPL--PLSKYRDCQFSFAGLKNTATR
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401 AA; 43849 MW; CC9426723D3FD4F1 CRC64;
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                                                                                                                                                                                                    32.7%; Score 453.5; DB 2; Length 401; 38.4%; Pred. No. 1.9e-30;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                 Mismatches 109;
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Best Local S
Matches 100
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A Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
A Champe M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
A Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K
A Yu C., Lewis S.E., Rubin G.M., Celniker S.,
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL, AVOS1882; AAK93306.1; -
R EMBL, AVOS1882; ARK93306.1; -
R FlyBase; FBgn0031066; CG14231.

R GO; GO:0008450; F:O-sialglycoprotein endopeptidase activity; IEA
R GO; GO:0008508; F:Orsialglycoprotein endopeptidase activity; IEA
R GO; GO:0008508; F:Droteolysis and peptidolysis; IEA.
R GO; GO:0008508; P:Droteolysis and peptidolysis; IEA.
R GO; GO:0008509; P:Droteolysis and peptidolysis; IEA.
R GO; GO:0008514; P:Droteolysis and peptidolysis; IEA.
R InterPro; IPR000905; Peptidase M22.
R InterPro; IPR000905; Peptidase M22.
R PIRSF; PIRSF004537; Osialglc pptds; 1.
R PRINTS; PR00789; OSIALOPPASE.
R PRINTS; PR00789; OSIALOPPASE.
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01-DEC-2001
01-DEC-2001
01-MAR-2004
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygol
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                       Similarity
ASTRYDYD---SIDIQGSAGFA
                                                           RRLSLIKHPECSTMSGGKAIEHLAK-QGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKII 117
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                                                                                                                             RARERAERTPPDGVISNYGDFCAGLLRSVSRHLMHRTQRAIEYCLLPHRQLFGDTPPTLV
                                                                                                                                                         MKKEKEEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILEC--KQRDLLPQNNAVLV 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HDIEGIRYEPKCPLGVDISKEVGEASIKVPQLKMEI 267
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                               -GIRYBPRCPLGVDISKEVGKA
                                                                                                                                                                                          RRLRLHILPEYRLWNGGRAIEHAAQLASDPLAYEFPLPLAQQRNCNFSFAGIKNNSFRAI 169
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1 (TrEMBLrel. 19,
4 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                      323 AA;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                  Score 415.5; DB 2;
Pred. No. 2.7e-27;
3; Mismatches 104;
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RA Mamatides P.G., Scherer S.E., Holt R.A., Evans C.A., Galle R.F.,
RA Mamatides P.G., Scherer S.E., Holt R.A., Evans C.A., Galle R.F.,
RA George R.A., Levis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Dutler H., Cadleu E., Center A., Chandra I.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Golden K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Goldek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.I., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.I., Harvey D., Helman T.J., Wei M.H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Liang Y., Lin X.,
RA Harris N.I., Mushina N.V., Mobarry C., Morris J., Moshreti A.,
RA Mcim J.R., Woldira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshreti A.,
RA Melson D.R., Nalson K.A., Nixon K., Nixoskern D.R., McCherson D.L.,
RA Melson D.R., Nalson K.A., Nixon K., Nixoskern D.R., Shien H.,
RA Shue B.C., Siden-Kiamos I., Singson M., Skupski M.P., Smith T.,
RA Sheng X.H., Mordaget M., Zhang G., Zhao Q., Ye J.,
RA Sheng X.H., Zhong F.N., Zhang W., Zhang S., Zhu X., Smith H.O.,
RA Sheng X.H., Sand G., Shang M., Shang S., Zhu X., Smith H.O.,
RA Sheng X.H., Shang
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01-MAY-2000 (TrEMBLrel. 1:
01-MAR-2004 (TrEMBLrel. 26
CG14231-PA.
OPEN---
                                                                                                                                            MEDLINE=22426065; PubMed=12537568;
Celniker S.B., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren B.J., Svirskas R., Tabor P.B., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.B., Myers B.W., Gibbs R.A., Rubin G.M.; "Finishing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence."; Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., C:
Patel S., Frise B., Wheeler D.A., Lewis S.B.,
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Adams M.D., Celniker
Amanatides P.G., Sche
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NCBI_TaxID=7227;
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   Carlson J.,
Rubin G.M.
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Best Local Simi
Matches 100;
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GO:0008508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR000905; Peptidase M22.
InterPro; IPR009180; Pept M22 Osialgl.
Pfam; PP00814; Peptidase M22; 1.
PIRSF; PIRSF004537; Osialglc pptds; 1.
PRINTS; PR00789; OSIALOPTASE.
PRODOR; PD00789; OSIALOPTASE.
PRODOR; PD00789; OSIALOPTASE.
               O22145; Q8VWL2;
01-JAN-1998 (TrEMBLrel. 05,
01-JUN-2002 (TrEMBLrel. 21,
05-JUL-2004 (TrEMBLrel. 27,
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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B.,
Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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                                                                               022145
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FlyBase; FBgn0031060; CG14231.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (SEP-2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The transposable elements of the Drosophila me
a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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 O-sialoglycoprotein
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                                                                              PRELIMINARY;
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45328 MW; 9797F66E7D155538 CRC64;
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Best Local
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EMBL; AY074338; AAK00530.1; -.
EMBL; AY073864; AAL35220.1; -.
EMBL; AY117283; AAM51358.1; -.
PIR, E84888; E84888
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Submitted
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Town C.D.
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GO; GO:0008450; F:O-sialoglycoprotein endopeptidase GO; GO:0008233; F:peptidase activity; IEA.

GO; GO:0008270; F:zinc ion binding; IEA.

GO; GO:0008270; F:zinc ion binding; IEA.

InterPro; IPR000905; Peptidase M22.

InterPro; IPR00190; Peptidase M22.

InterPro; IPR00190; Pept M22 GW13191.

PERMS; PR001814; Peptidase M22; I.

PIRSF; PRO018157; OSIALGEC DPtd8; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M., Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones Kamiya A., Karlin Neumann G., Kawai J., Kim C., Lam B., Lin J., Kamiya A., Karlin Neumann G., Kawai J., Kim C., Lam B., Lin J., Satou Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou Seki M., Shinn P., Southwick A., Shinnozaki K., Davis R.W., Ecker
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Arabidopsis thaliana (Mouse-ear Cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core everosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00789; OSIALOPTASE
ProDom; PD002367; Peptidase_N
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                                                                                                                                                                                                                                                                                                                                                           TIGRFAMs;
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                                                                                                                                                                                                                              Similarity
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1 K., Adamska I.;
WLGLDMH---
                                                                                                                               MEAHALTIRLT-NKVEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVAR
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                                             RLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMK
                                                                                                    MEAHALVARLVEQELS PPFMALLISGGHNLLVLAHKLGQYTQLGTTVDDAIGEAFDKTAK
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                                                                                                                                                                                                                                                                                                        480 AA;
                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                           Peptidase_M22; 1.
29; gcp; 1.
--RSGGPAVEELALEGDAKSVKFNVPMKYHKDCNFSYAGLKTQVRLAIEA
                                                                                                                                                                                                                                                                                                        52995 MW;
                                                                                                                                                                                                                            29.4%;
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                                                                                                                                                                                                    Score 407.5; DB 2
Pred. No. 2.1e-26;
7; Mismatches 93
                                                                                                                                                                                                                                                                                                        20DD6A86ACC1FFAD CRC64;
                                                                                                                                                                                                      93;
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Best Local S
Matches 84
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Brownlie J.C., McGraw E.A., Martin W., Esser C., Ahmadinejad N.,
Wiegand C., Madupu R., Beanan M.J., Brinkac L.M., Daugherty S.C.,
Durkin A.S., Kolonay J.F., Nelson W.C., Mchamoud Y., Lee P.,
Berry K.J., Young M.B., Utterback T.R., Weldman J.F., Nierman W.C.,
Paulsen I.T., Nelson K.E., Tettelin H., O'Neill S.L., Eisen J.A.,
"Phylogenomics of the reproductive parasite Wolbachia pipientis wMel:
a streamlined genome overrun by mobile genetic elements.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0008450; F:O-sialoglycoprotein endopeptidase GO; GO:0008270; F:zinc ion binding; IEA. GO:0008270; F:zinc ion binding; IEA. GO:0006508; P:proteolysis and peptidolysis; IEA. InterPro; IPR000905; Peptidase M22. InterPro; IPR009180; Pept M22 Osialgl. Pfam; PF00814; Peptidase M22; 1. PIRSF; PIRSF004537; Osialglc_pptds; 1. PRINTS; PR00789; OSIALOPTASE. PRODOM; PD002367; Peptidase M22; 1.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome. SEQUENCE 335 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLOS Biol. 2:327-341(2004).
EMBL; AE017258; AAS14395.1; -.
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Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Wolbachieae; Wolbachia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGRFAMs; TIGR00329;
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                                                                                                                                                                                                                   EKEEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGV
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AANNFLREKLKOHIN---LNIFFPPNDLCTDNAIMVGWTGIERLOKNY--
                                                                ASNETITARALETETNATOCTALCPPPRICTONGIMIAWNGIERLRAGIGILHDIEGIRYE 240
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Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882 (2001).

REMEL; AL1591792; CAC47657.1;
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0016787; F:chydrolase activity; IEA.
GO; GO:0008450; F:o-sialoglycoprotein endopeptidase act
GO; GO:0008270; F:zinc ion binding; IEA.
GO; GO:0008589; P:proteolysis and peptidolysis; IEA.
InterPro; IPR000905; Peptidase M22.
InterPro; IPR009180; Peptidase M22.
InterPro; IPR009180; Peptidase M22; 1.
PIESF; PIESF004537; Osialglc. pptds; 1.
PIESF; PR00789; OSIALOPTASE.
PRINTS; PR00789; OSIALOPTASE.
PTIGRPAMS; TIER00329; acc. 1.
PTIGRPAMS; TIER00329; acc. 1.
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TIGRAMS; TIGRO0329, gcp; 1.
Complete proteome; Hydrolase.
TOTTENER 360 AA; 37906 MW;
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Q92LH8; Q92LH8; Q1-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLYCEL. 26, Last annotation update)
PROBABLE O-SIALOGLYCOPROTEIN ENDOPEPTIDASE (EC 3.4.24.57).
ORFNames=SMC03230;
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secs
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35.6%; Pred. No. 3.5e-
tive 38; Mismatches
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## SUMMARIES

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## ALIGNMENTS

## RESULT 1 ABG96487 ID ABG96487 AC ABG9 XX ABG9 XX ABG9 XX Nove XX Meta XW Meta XW Meta XW Park XW Park XW Park XW emphi XW emphi XW emphi XW W020 XW W020 XW 19-S XX HOMC XX W02-F XX W02-F XX W02-F XX W01-F XX W01-F XX WPI; DR N-PS XX New PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac PT Treac Metalloprotease; MP-1; immune disorder; glutamate transport; cancer; motor neuron disorder; amyotrophic lateral sclerosis; ALS; diabetes; reproductive disorder; Kelinfelter's syndrome; germinal cell aplasia; genital wart; metabolic disorder; premature puberty; Kallman syndrome; cushing's syndrome; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; Huntington's disease; Tourette syndrome; sepsis; liver disease; renal disease; immune disorder; rheumatoid arthritis; acquired immunodeficiency syndrome; AIDS; pulmonary disease; pneumonia; Homo sapiens. emphysema; cystic fibrosis; vascular disorder; inflammatory disorder; neurological disorder. Novel human metalloprotease MP1 fragment #1. 11-DEC-2002 ABG96487; ABG96487 standard; protein; (first entry) 267 ₿

WO200272751-A2

19-SEP-2002.

05-FEB-2002; 2002WO-US003353.

05-FEB-2001; 10-APR-2001; 2001US-0266518P. 2001US-0282814P.

(BRIM ) BRISTOL-MYERS SQUIBB CO.

Chen J, Peder J, Nelson TC, Duclos 'n

Krystek

S

N-PSDB; 2002-723329/78. ABS76639.

New isolated nucleic acid encoding MP-1 protein, useful for preventing, treating, or ameliorating diseases associated with aberrant metalloproteinase activity, e.g. immune, metabolic, inflammatory and neurological disorders.

Claim 5; Page 29; 473pp; English.

The invention describes an isolated nucleic acid molecule (I) encoding metalloprotease (MP-1). (I) is useful for preventing, treating, or

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Matches 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Metalloprotease; MP-1; immune disorder; glutamate transport; cancer; motor neuron disorder; amyotrophic lateral sclerosis; ALS; diabetes; reproductive disorder; Kleinfelter's syndrome; germinal cell aplasia; genital wart; metabolic disorder; premature puberty; Kallman syndrome; Cushing's syndrome; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; Huntington's disease; Tourette syndrome; sepsis; liver disease; renal disease; immune disorder; rheumatoid arthritis; acquired immunodeficiency syndrome; ADS; pulmonary disease; pneumonia; emphysema; cystic fibrosis; vascular disorder; inflammatory disorder; neurological disorder.
                                                                                                                                    05-FEB-2001; 2001US-0266518P.
10-APR-2001; 2001US-0282814P.
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                                                   (BRIM ) BRISTOL-MYERS SQUIBB CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
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Pred. No. 7.9e-131;
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Best Local S
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                                                                                             24-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or sepsis), pulmonary diseases (e.g. pneumonia, emphysema or cystic fibrosis) and vascular, inflammatory and neurological disorders (e.g. Alzheimer's disease or Parkinson's disease). This is the amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid encoding MP-1 protein, useful for preventing, treating, or ameliorating diseases associated with aberrant metalloproteinase activity, e.g. immune, metabolic, inflammatory and
                                 19-APR-2000; 2000CN-00106834
                                                                                                                                                             CN1318550-A.
                                                                                                                                                                                                                               Homo
                                                                                                                                                                                                                                                                                     Human; O-sialoglycoproteinase-like protein; OSGPLP; enzyme
                                                                                                                                                                                                                                                                                                                                                    Human O-sialoglycoproteinase-like protein SEQ ID NO:2
                                                                                                                                                                                                                                                                                                                                                                                                                       19-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTDNGIMIAWNGIERLRAGLGILHDIEGIRYEPKCPLGVDISKEVGEASIKVPQLKMEI 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1240; DB 5; ilarity 100.0%; Pred. No. 1.5e-130; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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Best Local S
Matches 239
                                                                                                                                                                                                                                     cerebroprotective; antiparkinsonian; nootropic; antiinflammatory; antiulcer; hepatotropic; gynaecological; antibacterial; virucide; protozoacide; antiparasitic; cell proliferative disease; PMOD; protein modification and maintenance molecule; immunogenic fragment; cancer; autoimmune; inflammatory disease; neurological disorder; gastrointestinal; developmental; vesicle trafficking disorder; infect protein-protein interaction; drug-target interaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents human O-sialoglycoproteinase-like protein (OSGPLP). The present invention also describes: (1) the preparation of the OSGPLP protein; (2) applying the OSGPLP protein in diagnosis; (3) the prevention and/or treatment of related diseases; (4) utilising the OSGPLP protein in screening its agonist, excitomotor and inhibitor and preparing an antibody against the OSGPLP protein; and (5) the use of the OSGPLP polynucleotide sequences, proteins, agonists, excitomotors, inhibitors and antibodies in treating diseases related to the abnormal OSGPLP gene and in preparing the medicine composite for the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O-sialogycoproteinase-like for diagnosing, preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytostatic; antiarteriosclerotic; anti-HIV; antiallergic; anticonvulsant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABJ26654 standard; protein; 414 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 414 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein modification + maintenance molecule protein SEQ ID
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Pred. No. 1.5e-130;
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06-JUL-2001; 2001US-0303445P.
13-JUL-2001; 2001US-0305405P.
09-AUG-2001; 2001US-0311442P.
24-AUG-2001; 2001US-0314821P.
29-AUG-2001; 2001US-0315992P.
03-MAY-2002; 2002US-0378205P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Porsythe r.,
Thangavelu K, Gr.,
Thangavelu K, Gr.,
Thangavelu K, Mason PM, F
                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated human PMOD polypeptide and polynucleotide, useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant PMOD expression, e.g. cancer, AIDS, atherosclerosis
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N-PSDB; ABT23207.
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                                                               HPDI KPPLHHAKNCDFSFTGLQHVTDKI IMKKEKBEGI EKGQILSSAADI AATVQHTMAC
                                                                                                                                                                                                                                                                  414 AA;
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                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                              Score 1240; DB 6;
Pred. No. 1.5e-130;
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                    New 38650, 28472, 5495 useful for diagnosing hematopoietic, brain,
                                                                                                                                                             08-NOV-2000; 2000US-0246768P.
08-NOV-2000; 2000US-0246772P.
15-NOV-2000; 2000US-0249185P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human glycoprotease 28472 protein.
                                                                          N-PSDB; AAD46856.
                                                                                                               Leiby
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                                                                                                                                      (MILL-) MILLENNIUM PHARM INC
            pharmacogenomics.
                                                                                       2002-759898/82
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                                                                                                               줐
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                                                                                                             Kapeller-Libermann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Non-transmembrane domain; N-terminal cytoplasmic domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "Non-transmembrane domain;
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                                                                                                                                                                                                                                                                                                                                                               "Non-transmembrane domain; cytoplasmic
                                                                                                                                                                                                                                                                                                                                         "Transmembrane domain"
                                                                                                                                                                                                                                                                                                               "Non-transmembrane domain"
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                                                                                                               Glucksmann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 232
                                                                                                                                                                                                                                    cancer; aberrant cell proliferation; aberrant cell differentiation; breast cancer; ovarian cancer; prostate cancer; cardion cancer; lung cancer; immune disorder; heart disorder; cardiovascular disorder; endothelial disorder; hematopoietic disorder; blood vessel disorder; brain disorder; pain; metabolic disorder; liver disorder; diabetes; platelet disorder; carcinoma; sarcoma; leukaemia; Hodgkin's disease; autoimmune disorder; hypertension; atherosclerosis; heart failure; myocardial infarction; ischaemic heart disease; Crohn's disease; Grave's disease; Kawasaki syndrome; Raynaud's disease; aneurysm; cerebral ischaemia; peripheral neuropathy; Alzheimer's disease; envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence envergence e
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                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human glycoprotease 28472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTDNGIMIAWNGIERLRAGLGILHDIEGIRYEPKCPLGVDISKEVGEASIKVPQLKMEI 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HLVKRTHRAILFCKQRDLLFQNNAVLVASGGVASNFYIRRALBILTNATQCTLLCPPPRL
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                                                                                                                                                                                                                     disease;
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Pred. No. 2.3e-126;
                                                                                                                                                                                                                     nervosa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorder;
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Domain

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Glycoprotease\_domain

Location/Qualifiers

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                                                                                                                                                                                                                                                                                                                                                                                                                      The invention describes isolated 38650, 28472, 5495, 65507, 81588 and CC 14354 nucleic acid molecules (I) and their encoded polypeptides (II). The CC 38650 nucleic acid molecule comprises a sequence encoding adenosine CC deaminase. The 28472 nucleic acid molecule comprises a sequence encoding CC a human glycoprotease. The 5495, 65507, 81588 and 14354 comprise CC sequences that encode a human seven transmembrane domain (7TM). The CC 38650, 28472, 5495, 65507, 81588 or 14354 nucleic acid and polypeptide CC sequences are useful for diagnosing, preventing or treating a subject CC with or at risk of developing a disorder, e.g. cancer or aberrant CC cellular proliferation and/or differentiation (e.g. breast, ovarian, CC prostate, colon or lung cancer), immune disorders, heart disorders, cardiovascular disorders, endothelial disorders, heart disorders, CC blood vessel disorders, brain disorders, pain and metabolic disorders, CC liver disorders or platelet disorders. These disorders include carcinoma, CC sarcoma, leukaemia, Hodgkin's disease, autoimmune disorders (CC syndrome, Raynaud's disease, Crohn's disease, Grave's disease, Kawasaki CC syndrome, Raynaud's disease, aneurysm, cerebral ischaemia, peripheral cc cachexia or diabetes. This is the amino acid sequence of the novel human crowners are 28479.
                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New adenosine deaminase, glycoprotease and seven transmembrane nucleic acids and polypeptides, designated 38650, 28472, 5495, 81588 and 14354, useful for treating e.g. leukemias, Hodgkin's
                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Fig 8A-B; 178pp; English.
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08-NOV-2000; 2000US-0246772P.
15-NOV-2000; 2000US-0249185P.
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                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                         296
                                                                                                            121
                                                                                                                                                                                                                            176
356
                                181
                                                                                                                                                                  61 HPDIKPPLHHAKNCDPSFTGLQHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMAC 120
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                                                                                                                                                                                                                                            1 LLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRF 60
                                                                                          HLVKRTHRAILFCKORDLLPONNAVLVASGGVASNFYIRRALEILTNATOCTLLCPPPRL 180
                 CTDNGIMIAWNGIERLRAGLGILHDIEGIRYEPKCPLGVDISKEVGEASIKVPQLKMEI 239
                                                                                                                                                                                                                                                                                                                                                                           414 AA;
                                                                                                                                                 HFDIKPPLHHAKNCDFSFTGLQHVTDKNNENRKQBEGIEKGQILSSAADIAATVQHTMAC
                                                                                                                                                                                                                          LLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kapeller-Libermann R,
                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                   97.0%;
97.1%;
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                                                                                                                                                                                                                                                                                                                   Score 1203; DB 6;
Pred. No. 2.3e-126;
                                                                                                                                                                                                                                                                                                  Mismatches
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65507,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disease or
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ABU09569 ID ABU0

ABU09569

standard; protein;

414

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HPDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMAC

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                                                                                                                                      The invention relates to an isolated 38650 (encoding adenosine CC deaminase), 28472 (encoding a glycoprotease), 5495 (encoding a 7 CC transmembrane receptor), 65507, 81588 or 14354 nucleic acid molecule (or CC transmembrane receptor), 65507, 81588 or 14354 nucleic acid molecule (or CC a sequence which is at least 60% identical to the six nucleic acids or CC naturally occurring variants, or a DNA insert of the plasmid deposited CC with the American Type Culture Collection as Accession No. not defined in CC the specification, which encodes the amino acid sequence). Also included CC are a host cell containing the nucleic acids (used to produce the CC troteins), the encoded proteins, an antibody that selectively binds to CC the polypeptide, and identifying a compound that binds to/modulates the CC activity of the polypeptide. The nucleic acid molecules, polypeptides and CC methods are useful for diagnosing, treating cancer, aberrant cellular CC cardiovascular disorders including endothelial cell disorders, pain CC cardiovascular disorders, liver disorders and platelet disorders pain and metabolic disorders, liver disorders and platelet disorders (many CC examples of these disorders are given in the specification). The present
                                                                                  Query Match
Best Local
                                                                     Matches
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08-NOV-2000;
15-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Fig 8; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; enzyme; cancer; aberrant cellular proliferation; differenti immune disorders; heart disorder; brain disorder; cardiovascular disorder; endothelial cell disorder; pain disorder; haematopoeitic disorder; blood vessel disorder; metabolic disorder liver disorder; platelet disorder; glycoprotease.
                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated 38650,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-NOV-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  molecules, useful
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   317
                                                                     232;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             olated 38650, 28472, 5495, 65507, 81588 and 14354 nucleic acid les, useful for diagnosing, treating cancer, pain, or immune, endothelial cell, hematopoeitic, blood vessel, brain, metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEIBY K R.
KAPELLER-LIBERMANN
GLUCKSMANN M A.
                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACA60887.
LLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRF
                                                                                                                                      414
                                                                                                                                                                     is the Human glycoprotease encoded by cDNA 28472
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                                                                    Conservative
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2000US-0246772P.
2000US-0249185P.
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                                                                                  97.0%;
97.1%;
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                                                                  Score 1203; DB 6;
Pred. No. 2.3e-126;
3; Mismatches 4;
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                                                                                                 Length 414;
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                                                                    Gaps
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                                                                                                                                        Query Match
Best Local S
Matches 186
                                                                                                                                                                                                               The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
                                                                                                                                                                                                                                                                                                               New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases which the gene is involved, or as target molecules for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-395539/38.
N-PSDB; ADA52832.
                                                                                                                                                                                                                                                                                                                                                                                                       Isogai T, Sugiyama T,
Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic; Gene Therapy; human; secretory protein; membrane proteins; cancer; inflammatory disease; osteoporosis; neurological disease.
                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                         Claim 14; SEQ ID NO 2039; 205pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-SEP-2001; 2001JP-00328381.
24-JAN-2002; 2002US-0350435P.
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(REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                     Local Similarity
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               121
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                                                                                                                                          186;
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HLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRALEILTNATQCTLLCPPPRL
                                                               HFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMAC
                                                                                       LLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRF
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                                                                                                                                                                                         364 AA;
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Hio Y, Otsuka K, Nagai K, Irie R,
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                       0; Mismatches
                                                                                                                                                    Score 960; DB 6
Pred. No. 5e-99;
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                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 83; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 409 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genes from Drosophila interactions.
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N-PSDB; ABL13236.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAR-2000; 2000US-0191637P
11-JUL-2000; 2000US-00614150
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                                                                                                       AYEFPLPLAQQRNCNFSFAGIKNNSFRAIRARERAERTPPDGVISNYGDFCAGLLRSVSR 286
                                                                                                                                                               HFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMAC
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HLMHRTQRAIEYCLLPHRQLFGDTPPTLVMSGGVANNDAIYANIEHLAAQYGCRSFRPSK 346
                                                     HLVKRTHRAILFC--KQRDLLPQNNAVLVASGGVASNFYIRRALEILTNATQCTLLCPPP 178
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                                                                                         Query Match
Best Local S
Matches 82
                                                                                                                                                                                           Proteins AAY52202-Y52217 encompass a novel family of proteins designated the ygjD family, after the name given to the Escherichia coli family member. These proteins are essential for the survival of both Gram negative and Gram positive bacteria, although no function has as yet been ascribed to these proteins. The ygjD proteins, fragments of ygjD proteins (for example, fragments encompassing one or more conserved ygjD motifs such as AAY52218-Y52284) and nucleotides encoding them can be used to identify antagonists and broad spectrum antibacterial compounds. These antagonists and compounds can be used to treat a wide range of bacterial infections. New antibiotics are urgently needed, as serious bacterial infections and antibiotic resistant strains are becoming increasingly prevalent. The proteins of the invention are essential proteins for bacterial viability, and represent new targets for antibiotics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ygjD protein; essential; Gram positive; Gram negative; conserved; motif; identification; antagonist; antibacterial; antibiotic; broad spectrum; treatment; infection; resistance; drug target.
                                                                                                                                                               Sequence 463 AA;
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                                                                                           82; Conservative
                                                                                                            Similarity
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                  RLCTDNGIMIAWNGIERLRAGLGILHDIE-GIRYEPKCPLGVDISKEVGEA
                                      LIALVGGVSDFILILGRSLDIAFGDMLDKVARRLSLIKHPECSTMSGGKAIKHLAKQGNRF 60
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208. .259
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                                                                                                          26.3%;
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                                                                                        Score 326; DB 3; Length 463; Pred. No. 2.6e-27; Mismatches 84; Indels
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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29-OCT-1999;
25-FEB-1999

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23-MAR-1999

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24-MAR-1999

06-APR-1999

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hybridisation assay; genetic mapping; gene expression control; promoter;
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28-OCT-1999;
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                               New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                 Claim 25; SEQ ID NO 50858; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAR-2002; 2002WO-US009107
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Trawick JD,
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Pred. No. 1.5e-26;
                                                                                                                                                                                                                                                                             Haselbeck R, Yamamoto R,
                                                                                                                                                                                                                                                                             Ohlsen
Forsyth
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Xu HH;
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The invention relates to an isolated nucleic acid comprising any one

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21-MAR-2002; 2002WO-US009107.

WO200277183-A2

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the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

((1) a vector comprising a promoter operably linked to the nucleic acid cenciding a polypeptide whose expression is inhibited by the antisense concleic acid; (4) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the cantisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation; (7) identifying a omegon required for proliferation, or that has an activity against a biological pathway in which a proliferation, or that inhibits cellular proliferation or the biological pathway in which a proliferation, or that inhibits gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of the strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for clentifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 382 AA;
                                                                                                                              Moraxella catarrhalis.
                                                                                                                                                                    Antisense; prokaryotic essential
                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                              19-JUN-2003
                                                                                                                                                                                                                                                                                                       ABU35232;
                                                                                                                                                                                                                                                                                                                                                  ABU35232 standard; protein; 348 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 20.7%;
Local Similarity 36.1%;
les 74; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 HLVKRTHRAILFCKORDLLPQNNAVLVASGGVASNFYIRRALEILTNATOCTLLCPPPRL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 FDIKPPLHHAKNCDFSFTGLQ-HVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 LALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFH 61
                                                                                                                                                                                                                 encoded by Prokaryotic essential gene #20759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTDNGIMIAWNGIERLRAGIGILHD 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLAAKAIRAL---KOTGL-----RRLVVAGGVGANALLRAHLARALKPLRAEAYFPPLSL 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YDLPRPMLHSGDLDFSFSGLKTAVLTRV--KAATRDGGELGE--QDRADLAAATQAAIVE 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LMLVDGVGRYELLGETLDDAAGEAFDKSAKLMGL-GYP-----GGPALARLAEQGDASR 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTDNGAMIAFAAAERVKAGLADLRE 363
                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 257; DB 6; L; Pred. No. 1.2e-19; 33; Mismatches 78;
                                                                                                                                                                         gene; cell proliferation; drug design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 382;
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(1) a vector comprising a promoter operably linked to the nucleic acid conding a polypeptide whose expression is inhibited by the antisense concleic acid; (4) a host cell containing the vector; (3) an isolated containing the vector; (3) an isolated containing the vector; (3) an isolated containing the vector; (3) an isolated containing the polypeptide by the containing the vector; (3) an isolated containing the polypeptide; (5) producing the polypeptide; (6) inhibited by the condition or the activity of a gene in an operon required for proliferation; (7) identifying a operon that influences the activity of the gene product or that has an activity against a biological pathway (containing a gene required for cellular proliferation or the biological pathway in which a proliferation, or that inhibits cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a compound that inhibits the condition of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required conditions or screening for homologous nucleic acids required conditions or screening for homologous nucleic acids required conditions or screening for homologous nucleic acids required conditions or acroemated acts are sequence attains. Sureus, S. typhimurium, C. pneumoniae or P. aeruginosa. The present sequence attained by one of the target prokaryotic essential genes. Note: The sequence data for this conditions in the probaryotic essential genes. Note: The sequence data for this conditions.
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Best Local S
Matches 66
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 348 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 25; SEQ ID NO 63156; 1766pp; English.
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181 CTDNGIMIAWNGIERLRAG 199
                                                                                               121 HLVKRTHRAILFCKQRDLLÞQNNAVLVASGGVASNFYIRRALBILTNATQCTLLCÞÞÞRL 180
                                                                                                                                                                                                                                                      147
                                                                                                                                                                                       61 HFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMAC 120
                                                                                                                                                                                                                                                                                     1 LLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRF 60
                                                                                                                                                                                                                                                                                                                                               66;
                                                                                                                                                                                                                                                                                                                                                                    Similarity
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Trawick JD,
                                                                                                                                                              AYELPRPMQH-KGLDPSPSGMKTAIHNLIKDTPNAQSDP----ATRADIAASPEYAVVD
                                                                                                                                                                                                                                                      MLVRADGVGVYQILGESIDDAVGECPDKTAKMLKL-PYP-----GGPNIEKLAKNGNPH 199
                                                                                                                                                                                                                                                                                                                                               Conservative
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                          20.0%; Score 248.5; DB 6; Length 348; 33.2%; Pred. No. 9.4e-19; tive 33; Mismatches 79; Indels 21
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                                                                   LVVAGGVSANOMLRRTLTETLRQIDASVYYAPTEL
                                                                                                                                                                                                                                                                                                                                             79; Indels 21;
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Xu HH;
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306 CTDNGAMIAYAGFCRLSCG 324

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Search completed: February 16, 2005, 13:05:57 Job time: 49.0598 secs

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Result
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0., Gapext 0.5
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1240
1 LLALVQGVSDFLLLGKSLDI.....
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

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           US-10-067-443-22
US-10-067-443-3
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US-99-540-236-2726
US-99-543-681A-6513
US-99-549-39A-9921
US-99-409-03A-9921
US-10-067-443-4
US-10-067-443-5
US-08-087-797-2
US-08-087-797-2
US-08-087-797-12
US-08-087-797-148-5
US-09-10-279-728
US-09-710-279-728
US-09-710-279-728
US-09-710-279-728
US-09-710-279-728
US-09-710-279-728
US-09-710-279-73A-148
US-09-710-279-73A-148
US-09-134-010C-3909
US-09-583-3110-4857
US-09-138-352-4387
US-09-138-452A-213
US-09-138-452A-213
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           Sequence 22, Appli
Sequence 19, Appli
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Sequence 28, Appli
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atch cal s 239 29 61 61 121 121 149 181	SULT 1 Sequence 22, Application US/10067443 Sequence 22, Application US/10067443 Sequence 22, Application US/10067443 Sequence 22, Application US/10067443 Sequence 22, Application US/10067443 GENERAL INFORMATION: SQUENCE SQUENCE COMPATION: APPLICATION: FILLE REFERENCE: D0073 NP FILLE REFERENCE: D0073 NP CURRENT APPLICATION NUMBER: US/10/06 CURRENT FILING DATE: 2002-02-05 PRIOR APPLICATION NUMBER: US 60/266, PRIOR FILING DATE: 2001-02-05 PRIOR PRIOR APPLICATION NUMBER: US 60/282, PRIOR FILING DATE: 2001-04-10 NUMBER OF SEQ ID NOS: 71 SOFTWARE: PatentIn version 3.0 SEQ ID NO 22 LENGTH: 267 TYPE: PRT ORGANISM: homo sapiens		148.5 148.5 94.5 94.5 89.5 89.5 81.6 81.7 79 79 79 79 79 78
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Length 267;  Indels 0; Gaps 0;  STMSGGKAIEHLAKQCNRF 60	NOVEL METALOPROTEASE HIGHLY EXPRESSED		Sequence 4956, Appli Sequence 6, Appli Sequence 81, Appl Sequence 5050, Ap Sequence 3197, Ap Sequence 13841, A Sequence 5, Appli Sequence 5, Appli Sequence 7, Appli Sequence 7, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli
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RESULT 2
US-10.067-443-2
; Sequence 2, Application US/10067443
; Patent No. 6642041
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company

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; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo &
US-10-067-443-2
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CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR PILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 2
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                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: homo
US-10-067-443-19
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Best Local Similarity
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                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                             SEQ ID NO 19
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
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NUMBER OF SEQ ID NOS: 71
SOPTWARE: PatentIn version 3.0
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TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
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                                                 61 HFDIKPPLHHAKNCDFSFTGLOHVTDKIIMKKEKEEGI------
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                   HFDIKPPLHHAKNCDPSFTGLQHVTDKIIMKKEKEEGIFLISKVEQINIPGLCLKIAAHF 295
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Pred. No. 2.3e-141;
0; Mismatches 1;
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NUMBER OF SEQ ID NOS: 3840
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RESULT 5
US-09-540-236-2726
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Best Local Similarity 33.6
GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARI
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
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CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR PILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
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PILE REFERENCE: D0073 NP
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TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED IN
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US-09-540-236-2726
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Sequence 6513, Application US/09543681A
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Best Local (
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FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: 1998-07-27
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                              TDNGAMIAYAGCORLLAG---QHDGPAISVQPRWPM 395
                                                                                                                                                                                                                                                                                         FVFPRPMTDRPGLDFSFSGLKTFTLM-TWQRCVEAGDDSEQ---TRCDIALAFQTAVVET 310
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                                                                                                                                                     TDNGIMIAWNGIERLRAGLGILHDIEGIRYEPKCPL 217
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33.8%; Pred. No. 1.3e-19;
34. Mismatches 87;
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RESULT 8
US-08-087-797-3
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TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-6513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 6513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                 NAME: Layton, Jr., Samuel G.
REGISTRATION NIMBER: 22207
REFERENCE/DOCKET NUMBER: 337.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 704 377 1561
                                                                                                        APPLICATION NUMBER: US/0
FILING DATE: 14-JUL-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                  MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                      STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 LISVTGIGEYTLLGESIDDÁAGBAFDKTÁKLLGL-DYP-----GGPVLSKMÁQQGVEGR 211
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                                                                                                                                                                                                                                                                                                                                    Charlotte
: No. 5543312th Carolina
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Lo, Reggie Y.C.
Abdullah, Khalid M.
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704 334 2014
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                                                                                                                                                                  US/08/087,797
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                         RESULT
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Matches
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LENGTH: 343
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAB FOR DIAGNOSTICS AND THERAPEUTICS
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nes 67; Conserv
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                                                                                                                        181 CTDNGIMIAWNGIERLRAGLGILHDIE-GIRYEPKCPL 217
                                                                                                                                                                                                      122 LVKRTHRAILFCKQRDLLPQNN-AVLVASGGVASNFYIRRALBILTNATQCTLLCPPPRL 180
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                                                                                                                                                                                                                                                                                                                               148 LISVTGIGQYELLGESIDDAAGEAFDKTAKLLGL-DYP-----GGPMLSKMASQGTEGR 200
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                                                                                CTDNGAMIAYAGMVRLQTGA----KAELGVTVRPRWPL
                                                                                                                                                                  LMIKCRRA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                  16.5%; Score 205; DB 4; Length 343; 30.3%; Pred. No. 1.7e-16;
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; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-067-443-4
                                                                                                                                                                    US-10-067-443-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-067-443-28
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PRIOR APPLICATION NUMBER: US 60/282,814
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APPLICANT: Bristol-Myers Squibb Company
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED IN
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT PELICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR PILING DATE: 2001-02-05
PRIOR PILING DATE: 2001-02-05
                                                                                                                                                                                                                                                                                                                           SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 28, Application US/10067443 Patent No. 6642041
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Best Local Similarity
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    Best Local Similarity 27.5
Matches 69; Conservative
                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                     TYPE: PRT ORGANISM: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                     LENGTH: 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 -RFHFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69;
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                                     16.2%; Score 201.5; DB 4; 27.5%; Pred. No. 6.3e-16;
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    48;
Mismatches
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                                                                                    Length 421;
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    Indels
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                                                                                                                                                                                                           HOLECULE TYPE: protein US-08-087-797-2
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Best Local (
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                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                            NAME: LAYTON, Jr., Samuel REGISTRATION NUMBER: 22807
REGISTRATION NUMBER: 3374
REFERENCE/DOCKET NUMBER: 3374
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Mellox
                                                                                                                                                                                                                                                                                                                                        TELEFAX: 704 334 2014 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,797
FILING DATE: 14-ULI-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: LO, Reggie x.c.
APPLICANT: Abdullah, Khalid M.
APPLICANT: Abdullah, Khalid M.
TITLE OF INVENTION: Pasteurella Ha
TITLE OF INVENTION: Cane and the [
                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acid
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NAME: Layton, Jr., Samuel G.
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Seltzer, Park & Gibson, P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                    TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Charlotte
STATE: No. 5543312th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                         142 LVKVDGVGQYELLGESIDDAAGEAFDKTGKLLGL-DYP-----AGVAMSKLAESGTPNR 194
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62 FDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMACH 121
                                                                                  2 LALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPBCSTMSGGKAIEHLAKOGNRFH 61
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                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                             325 amino acids
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                                                                                                                             Conservative
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/ENTION: 'Pasteurella Haemolytica
                                                                                                                                                                                                                                                        linear
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                                                                                                                         16.1%; Score 200; DB 1; Length 325; 31.6%; Pred. No. 6.5e-16; ative 25; Mismatches 91; Indels
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US-09-107-532A-6609
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US-09-107-532A-6609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNSY/AGENT INFORMATION:
NAME: ATINIELLO, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
REFERENCE/DOCKET NUMBER: GTC-012
TELEFOAM: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6609:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6609, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...363
SEQUENCE DESCRIPTION: SEQ ID NO: 6609:
                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOUNCE:
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 7310
                                                                     169 LVYMQEDGSYEIIGETRDDAAGEAYDKVGRVLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 ----VDTILIKCK-RALEQTGYKRLVMAGGVSANKQLRADLAEMMKKLKGEVFYÞRPQFC 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195 FKPPRPMTDRPGLDFSFSGLKTFAANTIKANLNENGELDEQ---TKCDIAHAPQQAV---
NAME/KBY:
LOCATION:
                                                                                               LALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQG-NRF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TDNGAMIAYTGFLRLK 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TDNGIMIAWNGIERLR 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRALEILTNATQCTLLCPPPRLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 363 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/107,532A FILING DATE: 30-Jun-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 Beaver Street
                                                                                                                                                         15.9%; Score 197; DB 4; 32.6%; Pred. No. 1.8e-15; ative 34; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENTEROCOCCUS
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AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                     ----SYPSGKEIDQLAHQGKDNY 221
                                                                                                                                                            64; Indels
                                                                                                                                                                                                   Length 363;
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                                                                                                                                                            32; Gaps
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PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILLING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 327
TYPE: PRT
ORGANISM: Thermotoga maritima
US-10-067-443-5
                                                                                                                                                                                                                                                                                                                                                                                                   US-08-987-121A-4
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                                                                                                                                                                                                                                                                      Sequence 4, Application US/08987121A
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hoskins, Jo Ann
APPLICANT: Tang, Joseph Chiqu-Chi
APPLICANT: Treadway, Patti Jean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 15.6%; Score 193.5; DB 4; Length 327; Best Local Similarity 28.9%; Pred. No. 4.2e-15; Matches 55; Conservative 38; Mismatches 68; Indels 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/10067443 Patent No. 6642041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: D0073 NP
                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Bli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
                                                                                                                                                                                                               APPLICANT: Tang, Joseph Chiou-Chung
APPLICANT: Treadway, Patti Jean
TITLE OF INVENTION: Streptococcus Pneumoniae Gene Sequence
TITLE OF INVENTION: GCP
COMPUTER READABLE FORM:
                                                                                                                                                                                                NUMBER OF SEQUENCES:
                       COUNTRY: U
ZIP: 46285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 AGYEKAKRGM 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  191 NGIERLRAGE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 SYNFSFAGLK---TSVLYFLQREKGYK-----VEDVAASFQKAVVDILVEKTFR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          273 DVLITKTLRA---C-----QNYPVKQLVVAGGVAANQGLREGLQAALSAKLPEVELVI 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222 HF--PRAMIHEDNYDFSFSGLKSAFINLVHNAQQRGEDLDKN------DLAASFQASVI 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 NCDFSFTGLQHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMACHLVKRTHRAILF 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CKQRDLLPQNNAV--LVASGGVASNFYIRRALBILTNATQCTLLCPPPRICTDNGIMIAW 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPPRLCTDNGIMI 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----LARNIGIRKIAFVGGVAANSMLREEVRKRAERWNYEVFFPPLELCTDNALMVAK 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHLVKRTHRAILFCKQRDLLPQNNAV--LVASGGVASNFYIRRALEILTNA--TQCTLLC 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPLRLCGDNAAMI 335
                                            U.S.
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; LENGTH: 336 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-987-121A-4
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Search completed: February 16, 2005, 13:10:26
Job time : 15.288 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/987,121A
PILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 15.3%; Score 190; DB 3; Local Similarity 31.1%; Pred. No. 1.2e-14; les 61; Conservative 32; Mismatches 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 317-276-3334
TELEPHONE: GRO ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: X-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
                                                                                           300
                                                                                                                                       182 TDNGIMIA----
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                                                                                                                                                                                                                           122 LVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRALEILTNATQCTLLCPPPRLC 181
                                                                                                                                                                                                                                                                          196 YDFPRAMIKEDNLEFSFSGLKSAFINLHHNAE-----QKGESLST-EDLCASFQAAVMDI 249
                                                                                                                                                                                                                                                                                                                                                                144 LVYVSEAGDYKIVGETRDDAVGEAYDKVGRVMGL-----TYPAGREIDELAHQGHDI-
                                                                                                                                                                                                                                                                                                                    62 FDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMACH 121
                                                                                                                                                                                                                                                                                                                                                                                                          2 LALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFH 61
                                                                                           GDNAGMIAYASVSEWN 315
                                                                                                                                                                                 LMAKTKKAL-----EKYPVK--TLVVAGGVAANKGLRERL--ATEITDVNVIIPPLRLC
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                                                                                                                                       -WN 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3; Length 336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         30;
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Result
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                            1213.5
1213.5
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seq length: 2000000000
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1: /cgn2_6/ptcdata/2/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptcdata/2/pubpaa/USO7_NEW_PUB.pep:*

3: /cgn2_6/ptcdata/2/pubpaa/USO6_NEW_PUB.pep:*

4: /cgn2_6/ptcdata/2/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptcdata/2/pubpaa/USO7_NEW_PUB.pep:*

6: /cgn2_6/ptcdata/2/pubpaa/USO7_NEW_PUB.pep:*

7: /cgn2_6/ptcdata/2/pubpaa/USO8_NEW_PUB.pep:*

8: /cgn2_6/ptcdata/2/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptcdata/2/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptcdata/2/pubpaa/USO8_PUBCOMB.pep:*
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Match
100.0
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97.9
97.9
97.9
97.9
27.2
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1240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LLALVQGVSDFLLLGKSLDI......DISKEVGEASIKVPQLKMEI 239
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
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                                                                                                                                                                                                                                                                                                                                                      DB
                  US-10-067-443-22

US-10-649-273-22

US-10-651-722-22

US-10-667-443-2

US-10-649-273-2

US-10-649-273-2

US-10-649-273-19

US-10-649-273-19

US-10-651-722-19

US-10-651-722-19

US-10-651-722-19

US-10-651-722-19

US-10-649-273-19

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US-10-651-722-19

US-10-651-722-19
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                                                                                                                                                                                                                                                                                                                                                 Description
                  Sequence 22, Appl
Sequence 22, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 19, Appli
Sequence 19, Appl
Sequence 19, Appl
Sequence 5, Appli
Sequence 5, Appli
Sequence 2039, Ap
Sequence 2039, Ap
Sequence 209259,
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199.5	201.5	201.5	201.5	201.5	201.5	206	206	206	207	207.5	208	210	211	212	213	213	224	224	228.5	231	231	239	241	247	248.5	254	257	270	326	326
16.1	16.2	•	16.2	16.2	٠	•	16.6	16.6	•	•	•	16.9	17.0	17.1	•	17.2	18.1	18.1	18.4	18.6	18.6	•	19.4		•	•	•	21.8	•	26.3
350	421	421	421	421	421	396	337	337	441	341	335	337	41	340	337	337	342	342	347	341	341	251	343	312	348	333	382	444	463	463
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e 536	Sequence 28, Appli	e 28,	е4,	e 28,	4	e 67198,	æ	_	æ	e 67993,	55404	781	e 26, App	e 68438,	æ		Sequence 58204, A	1104		e 662	1179	9, Appl	Ø			Sequence 25, Appl	æ	Sequence 113732,	e 3,	Sequence 3; Appli

## ALIGNMENTS

US-10-067-443-22

Sequence 22, Application US/10067443
Publication No. US20030082782A1
GENERAL INFORMATION:

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; SEQ ID NO 22
; LENGTH: 267
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-067-443-22
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Best Local Similarity
Matches 239; Conserva
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TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/667,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/268,814
PRIOR PILING DATE: 2001-04-10
NUMBER: OF SEQ ID NOS: 71
ROTENARE DESCRIPTION STATES (2011-04-10)
RUMBER: OF SEQ ID NOS: 71
                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.0
  121 HLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRALEILTNATQCTLLCPPPRL 180
                                                                                                                                                                                          239;
                                    29
                                                                                                                Conservative
                                                                                                                                                                                            100.0%; Score 1240; DB 14; Length 267; 100.0%; Pred. No. 1.8e-127; ative 0; Mismatches 0; Indels 0;
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CURRENT APPLICATION NUMBER: US/10/651,722
CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR PILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOPTWARE: PATENTIN VETSION 3.2
SEQ ID NO 22
SEQ ID NO 22
                                                                                                                                                                                                                                                                 US-10-551-722-22
; Sequence 22, Application US/10651722
; Publication No. US20040048302A1
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
; FILE REFERENCE: D0073 DIV
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; ORGANISM: homo
US-10-649-273-22
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US-10-649-273-22
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CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
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Publication No.
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TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
FILS REFERENCE: D0073 CNT
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No. US20040043407A1
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Pred. No. 1.8e-127;
D; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOPTWARE: PatentIn version 3.0
SEQ ID NO 2
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US-10-067-443-2
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 414
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                Local Similarity
 356
                                  181
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                                                                                                                                        236
                                                                                                                                                                                                          176 LLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRF
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CTDNGIMIAWNGIERLRAGLGILHDIEGIRYEPKCPLGVDISKEVGEASIKVPQLKMEI 239
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                                                                                      HLVKRTHRAILFCKORDLLPONNAVLVASGGVASNFYIRRALBILTNATQCTLLCPPPRL 180
                                                                                                                                        HFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKBEGIEKGQILSSAADIAATVQHTMAC
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Pred. No. 1.
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RESULT 5
US-10-649-273-2
; Sequence 2, Application US/10649273
; Publication No. US20040043407A1

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CURRENT APPLICATION NUMBER: US/10/649,273
CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR PILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 2
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                                                                                                                                                                              ; ORGANISM: Homo US-10-651-722-2
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                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/10651722
Publication No. US20040048302A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TIFILE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
FILE REFERENCE: D0073 DIV
CURRENT APPLICATION NUMBER: US/10/651,722
CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-10
                                                                                      Query Match
Best Local Similarity
Matches 239; Conserv
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APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
                                                                                                                                                                                                                                                                  SEQ ID NO 2
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Best Local Similarity
                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: D0073 CNT
                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                            LENGTH: 414
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    LLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRP
                        LIAUVGGVSDFIIIIGKSLDIAFGDMLDKVARKUSLIKHPECSTMSGGKAIEHIAKQGNRF 60
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Conservative (
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                                                                                                          100.0%;
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Pred. No. 3.4e-127;
0; Mismatches 0;
                                                                                      Score 1240; DB 15;
Pred. No. 3.4e-127;
; Mismatches 0;
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; ORGANISM: homo sapiens
US-10-067-443-19
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US-10-067-443-19
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Sequence 19, Application US/10649273

Publication No. US20040043407A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1

FILE REFERENCE: D0073 CMT

CURRENT APPLICATION NUMBER: US/10/649,273

CURRENT APPLICATION NUMBER: US 60/266,518

PRIOR APPLICATION NUMBER: US 60/266,518

PRIOR FILING DATE: 2001-02-05
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PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.0
SEQ ID NO 19
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19, Application US/10067443

Publication No. US20030082782A1

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLS OF INVENTION: SPINAL CORD, MP-1
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT BLING DATE: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-05
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90.2%;
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PRIOR APPLICATION NUMBER: US 10/067,443

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; ORGANISM: homo sapiens
US-10-651-722-19
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US-10-649-273-19
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PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR PRIOR PRILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-10
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Best Local Similarity
                                                                                                                                                                                                                                                                                                             SEQ ID NO 19
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PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
FILE REFERENCE: D0073 DIV
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Local Similarity 90.2%;
hes 238; Conservative
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HFDIKPPLHHAKNCDPSFTGLQHVTDKIIMKKEKEEGIFLISKVEQINIPGLCLKIAAHF 295
                                     HFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGI-----
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                                                                                                                                       Score 1213.5; DB 15, -- Pred. No. 3e-124;
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US-10-094-749-2039

Sequence 2039, Application US/10094749

Publication No. US20030219741A1

GENERAL INFORMATION:

APPLICANT: APPLICANT: APPLICANT:

SUGIYAMA, TOMOYASU OTSUKI, TETSUJI WAKAMATSU, AI SATO, HIROYUKI

APPLICANT: ISOGAI, TAKAO APPLICANT: SUGIYAMA, TO

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                                                                                                                                                                                                                                                                                                               Matches
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: 38650, 28472, 5495, 65507, 81588, AND
TITLE OF INVENTION: 14354 METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND ITTLE OF INVENTION: THEREOP
FILLE REFERENCE: 381552004900
CURRENT APPLICATION NUMBER: US/10/012,140
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: 60/246,768
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/246,772
PRIOR APPLICATION NUMBER: 60/246,772
PRIOR APPLICATION NUMBER: 60/246,772
PRIOR APPLICATION NUMBER: 60/246,772
PRIOR APPLICATION NUMBER: 60/249,185
PRIOR APPLICATION NUMBER: 60/249,185
PRIOR FILING DATE: 2000-11-15
NUMBER: OF SEQ ID NOS: 49
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APPLICANT: Kapeller-Libermann, I
APPLICANT: Glucksmann, Maria A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 414
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                 y Match 97.0%;
Local Similarity 97.1%;
                                    181
                                                                           296
                                                                                               121 HLVKRTHRAILFCKQRDLLÞQNNAVLVASGGVASNFYIRRALEILTNATQCTLLCÞÞÞRL 180
                                                                                                                                                    236 HFDIKPPLHHAKNCDFSFTGLQHVTDKNNENRKQBEGIEKGQILSSAADIAATVQHTMAC
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                                                                         HLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRALEILTNATQCTLLCPPPRL
                                                                                                                                                                                             HFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMAC 120
                                                                                                                                                                                                                                    LLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRF
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CTDNGIMIAWNGIERLRAGLGILHDIEGIRYEPKCPLGVDISKEVGEASIKVPQLKMEI
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Pred. No. 3.9e-123;
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APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTMARE: PATENTIN Ver: 2.1
SOFTMARE: DATENTIN Ver: 2.1
SEQ ID NO 2039
LENCTH: 364
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US-10-094-749-2039
                                    ; OTHER INFORMATION: Clone US-10-424-599-209259
                                                                                                                                                                                                                                                                                                                                                                                         US-10-424-599-209259; Sequence 209259; Application US/10424599; Publication No. US20040031072A1
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 209259
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Best Local Similarity
Matches 186; Conserv
Query Match
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                                                                                                                                                                                                                                 APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
PILE REFERENCE: 38-21(53223)B
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                                                                            PEATURE:
                                                                                            ORGANISM: Glycine max
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                                                                                                                                     LENGTH: 445
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YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
NAGAHARI, KENJI
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NAGAI, KEIICHI
IRIE, RYOTARO
TAMECHIKA, ICHIRO
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27.2%;
                                                    ID: PAT_MRT3847_3098C.1.pep
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Pred. No. 1.7e-96;
Score 337;
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DB 15;
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Length 445;
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US-10-649-273-3

Sequence 3, Application US/10649273 Publication No. US20040043407A1 GENERAL INFORMATION:

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US-10-067-443-3
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Best Local Similarity 33.6
Matches 82; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED IN
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT ENLIGHTON NUMBER: US/10/067,443
CURRENT APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-10
NUMBER: OF SEQ. ID NOS: 71
NUMBER: OF SEQ. ID NOS: 71
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433 RSEA 436
                                             225
                                                                                          383
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                                                                                                                                                                                 326
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                                                                                                                                                                                                                                                                         276 SVKENVEMKYHKDCNESYAGLKTQVRLAIEAKE-----IRNRADIAASFQRVAVL 325
                                                                                                                                                                                                                                                                                                                                                                   221 LLVLAHKLGQYTQLGTTVDDAIGEAFDKTAKWLGLDMH-----RSGGPAVEELALEGDAK 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       308 RIAVLHLEERCERAIQWALKMEPSIRH----LVVSGGVASNQYVRARLDMVVKKNGLQLVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 PPPRICTDNGIMIAWNGIERLRAGIGILHDIEGIRYEPKCP 216
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                                                                                                                                                                                                                                                                                                   61 HFDIKPFLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMAC 120
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                                                                                                                                  CTDNGIMIAWNGIERLRAGLGILHDIEGIRYB------PKCPLGVDISKE 224
                                             VGEA 228
                                                                                       CTDNGVMVAWTGLEHFRVG---
                                                                                                                                                                               HLBEKCERAIDWALB---LEPSIKHWVISGGVASNKYVRLRLNNIVENKNLKLVCPPPSL 382
                                                                                                                                                                                                                            HLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRALEILTNATQCTLLCPPPRL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26.3%; Score 326; DB 14; 33.6%; Pred. No. 1.1e-26;
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                                                                                          ---RYDPPPPATEPEDYVYDLRPRWPLGEEYAKG
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; TYPE: PRT ; ORGANISM: Arabidopsis thaliana US-10-651-722-3
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PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.2
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CURRENT APPLICATION NUMBER: US/10/649,273
CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
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                                                   Matches
                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                      SEQ ID NO 3
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TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
FILE REFERENCE: D0073 DIV
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TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
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                                                                                                                HLEEKCERAIDWALE---LEPSIKHWVISGGVASNKYVRLRLNNIVENKNIKLVCPPPSL
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                                                         CTDNGVMVAWTGLEHFRVG-----RYDPPPPATEPEDYVYDLRPRWPLGEEYAKG
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Search completed: February 16, 2005, 13:28:32 Job time: 140.464 secs

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Result
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-MODEL-frame+ p2n.model -DEV=xlh
-MODEL-frame+ p2n.model -DEV=xlh
-Q-/cgn2 1/USPTO_Spool/US10649273/runat 14022005 114702 16399/app query.fasta_1.1429
-DB=GenEmb1 -QFMT=fastap -SUPFIX=rge -MINMATCH=0.1 -LOOFCL=0 -LOOFEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS-human40.cdi -LIST=45
-DOCALIGN=200:-THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=50 -MINLEN=0 -MAXLEN=2000000000
-USER-US10649273 @CGN 1 1 8655 @runat 14022005 114702 16399 -NCFU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG SCORES=0 -MAIT -DSPBICCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Listing first 45 summaries
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Perfect score:
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## ALIGNMENTS

Alignment Scores: pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match:	TITLE JOURNAL FEATURES SOUTCE ORIGIN	SOURCE ORGANISM REFERENCE AUTHORS	AR541929 LOCUS DEFINITION ACCESSION VERSION
ores: larity: imilarity:	Zhang, J., Zh Wang, D. and Nucleic acid Patent: US 6 Loc /on /mc	Unknown. Unknown. Unclassified. 1 (bases 1 to 1416) Tang, Y.T., Zhou, P.,	AR541929 Sequence 177 from paten AR541929 AR541929.1 GI:53934009
2.24c-113 1240.00 100.00\$ 100.00\$ 100.00\$	Zhang, J., Zhao, Q.A., Yang, Y., Xue, A.J Wang, D. and Drmanac, R.T. Nucleic acids and polypeptides Patent: US 6743619-A 177 01-JUN-2004; Location/Qualifiers 11416 /organism="unknown" /mol_type="genomic DNA"	to 1416)	ir .
Length: Matches: Conservative: Mismatches: Indels:	<pre>Zhang,J., Zhao,Q.A., Yang,Y., Xue,A.J., Wenrman,T., Wang,JK., Wang,D. and Drmanac,R.T. Nucleic acids and polypeptides Nucleic acids and polypeptides Patent: US 6743619-A 177 01-JUN-2004; Location/Qualifiers 11416 /organism="unknown" /mol_type="genomic DNA"</pre>	Unknown. Unknown. Unclassified. 1 (bases 1 to 1416) Tang,Y.T., Zhou,P., Goodrich,R., Liu,C., Asundi,V., Ren,F.,	1416 bp DNA US 6743619.
239 0 0 0	enrman, T.,	Asundi, V.,	linear
	wang, J ĸ.,	Ren, F.,	PAT 08-OCT-2004

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Alignment
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                                                              1 (bases 1 to 1526)
Chen, J., Feder, J.N., Nelson, T.C., Krystek, S.R. and Duclos, F. Polynucleotides encoding a novel metalloprotease, MP-1
Patent: US 6642041-A 23 04-NOV-2003;
Location/Qualifiers
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                                                                                                                       1908 bp mRNA linear
Homo sapiens O-sialoglycoprotein endopeptidase-like
clone MGC:20293 IMAGE:4121450), complete cds.
BC011904
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1908)

Strausberg,R.L., Feingold, B.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D. Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
                                                                         Homo sapiens
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Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,D., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 28 Row: i Column: 22.
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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On Dec 19, 2003 this sequence version replaced gi:15080281.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (30-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg, R.
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/translation="MLILTKTAGVPFKPSKRKVYBPLRSPNFHPGTLFLHKIVLGIBT
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/db xref="LocusID:64172"
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/clssue_type="Muscle, rhabdomyosarcoma"
/clone_lib="NIH MGC_17"
/lab_host="DH10B-R"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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AR428803 2197 bp
Sequence 1 from patent US 6642041.
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                                                                               IleSerLysGluValGlyGluAlaSerIleLysValProGlnLeuLysMetGluIle 239
                                                                                                                                                                   GlyIleLeuHisAspIleGluGlyIleArgTyrGluProLysCysProLeuGlyValAsp 220
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MSGGKAI EHLAKQGNRFHFDI KEPLHKKNCD PSFTGLGHVTDKI IMKKEKEEGI EKG
QILSSAADI AATVQHTMACHLVKRTHBAILFCKQRDLLPQNNAVLVASGGVASNFYIR
RALEI LTNATQCTLLCPPPRLCTDNGIMIAWNGI ERLRAGLGI LHDI EGIRYEPKCPL
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Chen,J., Feder,J.N., Nelson,T.C., Krystek,S.R. and Duclos,F.
Polynucleotides encoding a novel metalloprotease, MP-1
Patent: US 6642041-A 1 04-NOV-2003;
Location/Qualifiers
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                                                          GlyIleLeuHisAspIleGluGlyIleArgTyrGluProLysCysProLeuGlyValAsp
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                                                                                         ArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyValAlaSerAsn
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AJ295148.1 GI:11071726
metallopeptidase; sialoglycoprotease.
Homo sapiens (human)
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Submitted (27-OCT-2000) Chen J.M., Note: The Babraham Institute,
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Leiby, K.R., Kapeller-Libermann, R. and Glucksmann, M. 38650, 28472, 5495, 65507, 81588 and 14354 methods of human proteins auses thereof Patent: WO 02074260-A 6 26-527 2002, Millennium Pharmaceuticals, Inc. (US)
                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; !
Mammalla; Butheria; Primates; Catarrhini; Hominidae;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                           Homo sapiens (human)
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                                                                                                                                                                                                                                GlyIleLeuHisAspIleGluGlyIleArgTyrGluProLysCysProLeuGlyValAsp
                                                                                                                                                                                                                                                                                                                                                                          CAAAATAATGCAGTACTGGTTGCATCTGGTGGTGTCGCAAGTAACTTCTATATCCGCAGA
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                                                                                                                                                                 ATATCAAAAGAAGTTGGAGAAGCTTCCATAAAAGTACCACAATTAAAAATGGAGATA
                                                                                                                                                                           IleSerLysGluValGlyGluAlaSerIleLysValProGlnLeuLysMetGluIle 239
                                                                                                                                                                                                                   GGCATTTTACATGACATAGAAGGCATCCGCTATGAACCAAAATGTCCTCTTGGAGTAGAC 1185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LeuLeuAlaLeuValGlnGlyValSerAspPheLeuLeuLeuGlyLysSerLeuAspIle
                                                                                                  CAAAATAATGCAGTACTGGTTGCATCTGGTGGTGTCGCAAGTAACTTCTATATCCGCAGA
                                                                                                                        GlnAsnAsnAlaValLeuValAlaSerGlyGlyValAlaSerAsnPheTyrIleArgArg
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 CysThrAspAsnGlyIleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeu
                                    GCTCTGGAAATTTTAACAAACGCAACACAGTGCACTTTGTTGTGTCCTCCTCCCAGACTA
                                                   AlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProProArgLeu
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RALEILTNATQCTLLCPPRICTDNGIMIAWNGIERLRAGLGILHDIEGIRYEPKCPL
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
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                                       Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,B., Kwong,P., Laric,P., Legaspi,R.,
Hansen,N., Ho,S.-L., Karlins,B., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Makeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDCwcll,J., Fearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus cDNA clone MGC:67870
BC058172
                                                                                                                                                                                                                                                          CDNA Library Preparation: Life Technologies, Inc. (CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (15-SEP-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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Direct Submission
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Mammalia; Eutheria; Rodentia;
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                           Zhang, L.-H. and Green, B.D.
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IMAGE:5012054,
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HisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuPro 140
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Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LeuLeuAlaLeuValGlnGlyValSerAspPheLeuLeuLeuGlyLysSerLeuAspIle
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21312463.
CTTCAACATATTACTGATAAGCTAATAACACACACAGGAAAAAGGAAGAAGGCATTGAGAAG
                                                                                                                             LeuGlnHisValThrAspLysIleIleMetLysLysGluLysGluGluGlyIleGluLys 100
                                                                                                                                                                                                                                                 HisPheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGly 80
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QILSSAADIAAAVQHATACHLAKRTHRAILFCKQKNLLSPANAVILVVSGGVASNLYIR
KALEIVANATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGVLHDVEDIRYEPKCPL
GIDISREVAEAAIKVPRLKMAL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="Unknown (protein for MGC:67870)"
/protein_id="AAH98172.1"
/db_xref=="GGI:34849664"
/translation="MLMLRRTAGAIPKPPKSKVYGFLRRESVHPRTLSCHKLVLGIET
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SCDDTGAAVVDETGNVLGEALHSQTQVHLKTGGIVFFVAQQLHERIOIQRIVESTLANS
RITESDLSAAVTIKFOLASLGVGUSFSLQLVNRFKKPIPHHMEBAHATTRAUNK
VEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECST
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possible chaperone activity [Posttranslational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modification, protein turnover, chaperones]"
/db_xref="CDD:COG0533"
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/clone="MGC:67870 IMAGE:5012054"
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/strain="CZECH II"
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                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
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RS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Willalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A.,
Villalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A.,
Villalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,
Bouffard, G.G., Blakesley, R.M., Touchman, J.M., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
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                                                                                                                                                           Direct Submission
Submitted (25-OCT-2002) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                22388257
12477932
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                              USA
NIH-MGC Project URL: http://mgc.nci.nih.
Contact: MGC help desk
                                                                                                                                                                                                                                                                   Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Butheria; Rodentia;
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US-10-649-273-2_COPY_176_414 (1-239) x BC038910 (1-1017)
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Steven Jones, Jennifer Agano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacquelline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
Michael Scott Zuyderduyn, Marco Marra.
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                                                                                                GlnAsnAsnAlaValLeuValAlaSerGlyGlyValAlaSerAsnPheTyrIleArgArg
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IRAK Plate: 86 Row: f Column: 12.
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/clone="IMAGE:5053559" 
/tissue type="Liver, normal. 
/clone_Tib="NCI_CGAP_Li9" 
/lab_host="DH10B"
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Location/Qualifiers
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Helix Research Institute (JP); Resea
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             | Cl;Gln:leLeuSerSerAlaAiaAspIleAlaAlaThrValGlnHisThrMetAlaCys 120
                                                                                                               CATTITGACATCAAACCTCCCTTGCATCATGCTAAAAATTGTGATTTTCCTTTTACTGGA 1108
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GGGCAAATCCTGTCTTCAGCAGCAGACATTGCTGCCACAGTACAGCACACAATGGCATGT 1228
                                                       CTTCAACACGTTACTGATAAAATAATAATGAAAAAGGAAAAAGGGAAGGTATTGAGAAG
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                             Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Yakikawa, E., Omura, Y., Abe, K., Kamahara, K., Katsuta, M., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hiraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Takeaka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Sojiya, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakeoe, H., Hishigaki, H., Watanabe, T., Sujyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, T., Sujyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, T., Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Yamada, K., Pujii, Y., Ozaki, K., Hixiji, T., Kobatake, N., Nakajama, M., Hata, H., Watanabe, T., Nakagawa, K., Okumura, K., Nakajama, M., Hata, H., Watanabe, M., Sasaki, M., Togashi, T., Nakagawa, T., Nakagawa, T., Ohama, K., Okumura, K., Nakajama, M., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nakajamo, J., Yamashita, R., Complete sequencing and characterization of 21,243 full-length human COWAs
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Nishi,T., Nakagawa,S., Senoh,A., Mizuguchi,H., Inagaki,H., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                        Genet. 36
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clone FEBRA2004592,
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highly similar
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Isogai,T., Otsuki,T. and Sugiyama,T.
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                                                                                                                HisPheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGly
LeuGlnHisValThrAspLy8IleIleMetLy8Ly8GluLy8GluGluGlyIleGluLy8 100
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SCDDTAAAVVDETGNVLGEAIHSQTEVHLKTGGIVFRAFQLHRENIQRIVGLAKJR
GVSPSDLSALATTIKPGLALSLGVGLSFSLOLVGQLKKPFIPHHMRAHATIKLTIK
VBFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLFLIKHPECST
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QILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNFCI R
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/db_xref="GI:16550167"
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/tissue_type="brain"
/clone_lib="FEBRA2"
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                                                                                                                                                                                                                                         RS. Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Schaefer, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Scheetz, T.E., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schmerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1409
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BC078974
                                 Direct Submission

Direct Submission

Submitted (02-AUG-2004) National Institutes of Health, Mammalian Submitted (02-AUG-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer General National Cancer Cancer Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                 2 (bases 1 to 1546)
Director MGC Project.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus
NIH-MGC Project URL: http://mgc.nci.nih.gov
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norvegicus cDNA clone
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IMAGE:7111906, partial
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Best Local Similarity:
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                                           81
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Howard Jacobs
CDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 943
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 182 Row: f Column: 6
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                        LeuGlnHisValThrAspLysIleIleMetLysLysGluLysGluGluGlyIleGluLys 100
                                                                                                                    HisPheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGly 80
                                                                                                                                                                                                              CysSerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPhe 60
                                                                                                                                                                                    TGTTCTACAATGAGTGGTGGGAAAGCTATAGAACATTTGGCCAAAGAAGGAAATAGATTC 848
                                                                                                                                                                                                                                                                                LeuLeuAlaLeuValGlnGlyValSerAspPheLeuLeuGlyLysSerLeuAspIle
CACTTIACTATCAATCCACCCATGCAGAATGCTAAGAACTGTGATTTTTCTTTTACGGGA 908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="mimisktagaiprpprsnvrgfirrpnvqpralfhhkulugiet
Scddtaaavudetgnulgealisqtevilktegivppvaqqlireniqriveraltak
Gverenia attikgellistyounqfkkpfifilhmeahaltirlthk
Vgfpplvllisgghcllaluggvsdplllgksudiapgdmldkvarrlslikhpecst
Vgfpplvllisgghcllaluqsvsdplllgksudiapgdmldkvarrlslikhpecst
Vgfpplvllisgghcllaluqsvsdplllgksudiapgdmldkvarrlslikhpecst
Vlsaaadughatachlakrthralibfcqqknllsplanglyir
Raggkaibhlakegnafhtlugbghasniyir
Raggkaibhaavqhatachlakrthralibfcqqknllsplanglyir
Vsgfkaibhlakrycthlitheblusyssthtvahsplasgsrganiqtsmcsctqtvymrtvrhtl
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/protein_id="AAH78974.1"
/db_xref="GI:50926880"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="Testis, rat
/clone_lib="NIH_MGC_237"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10116"
/clone="IMAGE:7111906"
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Tissue Procurement: Marcello Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
NNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradl
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (14-APR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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BC051211.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAGCTAACGCAGTATTAGTTGTGTCTGGAGGTGTTGCAAGTAACTTGTACATCCGAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACCTTGCGAAAAGAACACATCGTGCTATTCTGTTTTGCCAGCAGAAAAATTTGCTATCT 1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 1109)
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/clone="IMAGE:1327545"
/ticsuc_trre="Thymus_glaind, mouse="/clone_lib="soares_thymus_2NDMT"
/lab_host="DH10B"
                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                            organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:29881634
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RESULT 15
EX930694
LOCUS
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KEYWORDS
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                                       SOURCE
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Gallus gallus (chicken)
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata;
                                                                                   Gallus gallus finished cDNA, BX930694
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                                                                                                                                                                                                   GlnLeuLysMetGluIle 239
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                                                                                                                                                                                 CGATTAAAAATGGCACTT 876
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    Vertebrata; Euteleostomi;
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JOURNAL
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      514
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Direct Submission
Submitted (29-MAR-2004) Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: chickest@bms.umist.ac.uk
On Apr 1, 2004 this sequence version replaced gi:41631222.
BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence is from the BBSRC/Jundee/Nottingham/Sanger/Sheffield/UMIST cDNA collection, BBSRC/Jundee/Nottingham/Sanger/Sheffield/UMIST cDNA was prepared from a library constructed by Elizabeth Bosch. cDNA was prepared from RNA extracted from limbs, normalised, and poly A-trimmed. BCORI-NotI cut cDNA was then ligated into the vector. Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI Host: Escherichia coli DH10B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 860)
Boardman, P.E., Bonfield, J.K.,
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Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequencing project.
                                                                                                                                                                                                                                                           GlnAsnAsnAlaValLeuValAlaSerGlyGlyValAlaSerAsnPheTyrIleArgArg 160
                                                                                       HisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuPro
                                                                                                                                                  GlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrWetAlaCys 120
                                                                                                                                                                                                                LeuGlnHisValThrAspLysIleIleMetLysLysGluLysGluGluGlyIleGluLys 100
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                                                                                                                                                                                                                                                                                                                                                                                                       AlaProGlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGlu
                                                                     TĠĊCACAGCATGGCCGGGGGGAAGGCATAGAGCACCTGGCTCAAACCGGAGACTGGCAA 273
                                                                                                                                 GGGGAAATCCTGTCCTGCGTTAAGGACATCGCTGCTGCTGCACAGCACGTAGTGGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, H
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/clone_lib="CSEQCHN59"
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Matches:
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-MODEL-frame+_p2n.model -DEV=xlh
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-Q=/cgn2_1/USPTO_spool/US10649273/runat_14022005_I14702_16389/app_query.fasta_1.1429
-DB=N_Geneseq_16Dec04 -QFMT=fastap -SUPFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE-LOCAL -OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10649273_GCGN_1 1_1057_grunat_14022005_114702_16389 -NCPU=6 -ICPU=3
-NO_MMAD -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LOGLOG
-DEV_TIMEOUT=120 -WARN_INEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Command line parameters:
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     February 16, 2005, 13:09:32 ; Search time 455.139 Seconds (without alignments) 3108.540 Million cell updates/sec
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1240
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Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyright
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## SUMMARIES

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## ALIGNMENTS

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autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis; insulin-dependent diabetes mellitus; anaemia; thrombocytopaenia; wound; ulcer; burn; bone disorder; osteoporosis; osteoarthritis; stroke; fibrosis; reperfusion injury; infection; allergic rhinitis; asthma; coagulation disorder; cancer; tumour; inflammatory disease; septic shock; Crohn's disease; anaphylaxis; proliferation; chemotactic; differentiation; stem cell growth factor; haematopoiesis; chemokinetic; Human; gene; ss; nervous system disorder; peripheral neuropathy; Huntington's disease; amyotrophic lateral sclerosis; haemophilia; neurodegenerative disease; Parkinson's disease; Alzheimer's disease; haemostatic; antiinflammatory; expressed sequence

Homo sapiens.

WO200281731-A2

17-OCT-2002.

29-JAN-2002; 2002WO-US001222.

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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel polypeptide useful for treating neurodegenerative diseases, my or lymphoid cell disorders, bone disorders, mechanical and traumatic disorders, coagulation disorders, and inflammatory diseases.
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                         New isolated nucleic acid entreating, or ameliorating dimetalloproteinase activity,
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                                                                                                                                                                                                                                                                                          Pred. No.:
                                                                                                                                                                                                                                                                                                                      Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence encodes human O-sialoglycoproteinase-like protein (OSGPLP). The present invention also describes: (1) the preparation of the OSGPLP protein; (2) applying the OSGPLP protein in diagnosis; (3) the prevention and/or treatment of related diseases; (4) utilising the OSGPLP protein in screening its agonist, excitomotor and inhibitor and preparing an antibody against the OSGPLP protein; and (5) the use of the OSGPLP polynucleotide sequences, proteins, agonists, excitomotors, inhibitors and antibodies in treating diseases related to the abnormal OSGPLP gene and in preparing the medicine composite for the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O-sialogycoproteinase-like protein and encoding polynucleotide, useful for diagnosing, preventing and treating related diseases.
                                                                                                                                                                                                                                                                                                                                                                          Sequence 2058 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; Page 29-30 (Disclosure); 38pp; Chinese.
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                                   05-FEB-2002; 2002WO-US003353
                                                                                        19-SEP-2002.
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CC The invention describes an isolated nucleic acid molecule (I) encoding a metalloprotease (MP-1). (I) is useful for preventing, treating, or CC ameliorating a medical condition, particularly an immune disorder, an CC aberrant glutamate transport or motor neuron disorder, such as CC amyotrophic lateral sclerosis (ALS), its juvenile form or an ALS-like CC condition. The compositions and methods are also useful for diagnosing, CC prognosticating, treating, ameliorating and/or treating disorders (CC associated with MP-1 activity, e.g. diabetes, cancer, reproductive CC disorders (e.g. Kleinfelter's syndrome, genital warts, or germinal cell aplasia), metabolic disorders (e.g. premature puberty, Kallman syndrome, CC or Cushing's syndrome), neurodegenerative diseases (Alzheimer's disease, Puntington's disease or Tourette syndrome), liver CC and renal diseases and immune disorders (e.g. AIDS, rheumatoid arthritis CC or sepsis), pulmonary diseases (e.g. pneumonia, emphysema or cystic CC fibrosis) and vascular, inflammatory and neurological disorders (e.g. Alzheimer's disease Or Parkinson's disease). This sequence represents a metalloprotease MP1 polynucleotide
New isolated nucleic acid encoding MP-1 protein, useful for preventing, treating, or ameliorating diseases associated with aberrant metalloproteinase activity, e.g. immune, metabolic, inflammatory and
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 1A-C; 473pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurological disorders.
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10-APR-2001; 2001US-0282814P.
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DB; ABG96478.
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Sequence 2197 BP; 681 A; 441 C; 439 <u>ი</u> 636 T; 0 U; 0 Other;

Score: Alignment

5.98e-132 1240.00 100.00% 100.00% 100.00%

Conservative: Mismatches: Indels:

Gaps:

Length: Matches:

No.:

Percent Similarity:
Best Local Similarity:
Query Match:
DB: 밁 S 밁 ð 밁 Ś 밁 ð 밁 5 밁 8 US-10-649-273-2\_COPY\_176\_414 (1-239) x ABS76635 (1-2197) 121 101 996 936 876 816 756 81 41 61 21 HisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuPro GlyGlnI1eLeuSerSerAlaAlaAspI1eAlaAlaThrValGlnHisThrMetAlaCys LeuGlnHisValThrAspLysIleIleMetLysLysGluLysGluGluGlyIleGluLys HisPheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGly CysSerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPhe AlaProGlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGlu CIGITGGCATTAGTTCAAGGAGTTTCAGATTTTCTGCTTCTTGGAAAGTCTTTGGACATA LeuLeuAlaLeuValGinGlyValSerAspPheLeuLeuLeuGlyLysSerLeuAspIle TGCTCCACCATGAGTGGGGAAAGCCATAGAACATTTGGCCAAACAAGGAAATAGATTT 2197 239 0 0 100 815 140 995 80 935 60 875 40

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06-JUL-2001; 2001US-0303445P.
13-JUL-2001; 2001US-0305405P.
09-AUG-2001; 2001US-0311442P.
24-AUG-2001; 2001US-0318921P.
29-AUG-2001; 2001US-0315992P.
03-MAY-2002; 2002US-0378205P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytostatic; antiarteriosclerotic; anti-HIV; antiallergic; anticonvulsant; cerebroprotective; antiparkinsonian; nootropic; antiinflammatory; antiulcer; hepatotropic; gynaecological; antibacterial; virucide; protozoacide; antiparasitic; cell proliferative disease; PMOD; protein modification and maintenance molecule; immunogenic fragment; cancer; autoimmune; inflammatory disease; neurological disorder; gastrointestinal; developmental; vesicle trafficking disorder; infection; protein protein interaction; drug-target interaction;
New isolated human PMOD polypeptide and polynucleotide, useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant PMOD expression, e.g. cancer, AIDS, atherosclerosis
                                                                                                                         Gandhi AR, Kable AE, Swarnakar A, Hafalia AJA, Tran B, Duggan BM; Warren BA, Ison CH, Honchell CD, Nguyen DB, Lu DAM, Lee EA, Yue H; Forsythe IJ, Barroso I, Ramkumar J, Griffin JA, Li JY, Yang J; Thangavelu K, Gietzen KJ, Ding L, Baughn MR, Borowsky ML, Yao MG; Walia NK, Mason PM, Gururajan R, Lee S, Becha SD, Lee SY, Tran UK; Elliott VS, Luo W, Sprague WW, Tang YT, Lu Y, Zebarjadian Y;
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                                                                                                                                                                                                                                                        GENOMICS INC.
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     and
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CC rhe invention relates to an isolated polypeptide comprising: any of 28 cc sequences of 48-1256 amino acids; a natural amino acid sequence at least CC 90% identical to the 28 amino acid sequence, 94% identical to a sequence (CC of 703 or 267 amino acids, 96% identical to a sequence of 414 amino (CC acids, or 97% identical to a sequence of 422 amino acids, all given in (CC the specification; or a biologically active or immunogenic fragment of (CC in diagnosing, treating and preventing diseases or conditions associated (CC with the decreased expression of protein modification and maintenance (CC alterosclerosis), autoimmune/inclammatory diseases (e.g. cancer, (CC allergies), neurological disorders (e.g. stroke, Parkinson's disease, (CC allergies), gastrointestinal (e.g. ulcer, cirrhosis), reproductive (e.g. cendometriosis), developmental, vesicle trafficking disorders, and (CC infections (e.g. bacterial, viral, parasitic, proteozoal). These are also (CC sefully) in assessing the effects of exogenous compounds on the expression (CC fragments are useful in screening compounds for effectiveness as agonist (CC or antagonist of the polypeptides, or in altering the expression of the captering protein.protein interactions, drug-target interactions, and (CC or measuring protein.protein interactions, drug-target interactions, and (CC encoding a human PMOD protein of the invention
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2572 BP; 780 A; 489 ü 509 G; 794 T; 0 U; 0 Other;

140	H18LeuValLysArgInrH18ArgAlaIleLeuPheCysLysGlnArgAspLeuLeuPro	rgAlaileLeuPheCy	LLysArgThrH18A	HisLeuVa	121	Ş
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102		CAGACATTGCTGCCAC	CCIGTCTTCAGCAG	GGGCAAAT	969	망
120	GlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCys	laAspIleAlaAlaTh	eLeuSerSerAlaA	GlyGlnIl	101	ঠ
968		TAATAATGAAAAAGGA	CGTTACTGATAAAA	CITCAACA	909	рb
100	LeuGlnHisValThrAspLysIleIleMetLysLysGluLysGluGlyIleGluLys	leIleMetLysLysGl	8ValThrAspLysI	LeuGlnHi	81	Ş
908	CATTTTGACATCAAACCTCCCTTGCATCATGCTAAAAATTGTGATTTTTCTTTTACTGGA	TGCATCATGCTAAAAA	CATCAAACCTCCCT	CATTTTGA	849	DЪ
80	HisPheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGly	euHisHisAlaLysAs	pIleLysProProL	HisPheAs	61	Ş
848	TGCTCCACCATGAGTGGTGGGAAAAGCCATAGAACATTTGGCCCAAACAAGGAAATAGATTT	AAGCCATAGAACATTT	CATGAGTGGTGGGA	TGCTCCAC	789	рь
60	CysSerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPhe	ysAlaIleGluHisLe	rMetSerGlyGlyL	CysSerTh	41	ঠ
788	GCACCAGGTGACATGCTTGACAAGGTGGCAAGAAGAAGACTTTCTTT	AGGTGGCAAGAAGACT	TGACATGCTTGACA	GCACCAGG	729	DЬ
40	AlaProGlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGlu	ysValAlaArgArgLe	yAspMetLeuAspL	AlaProGl	21	ঠ
728	CTGTTGGCATTAGTTCAAGGAGTTTCAGATTTTCTGCTTCTTGGAAAGTCTTTGGACATA	TTTCAGATTTTCTGCT	ATTAGTTCAAGGAG	CTGTTGGC	669	DЬ
20	LeuLeuAlaLeuValGlnGlyValSerAspPheLeuLeuLeuGlyLysSerLeuAspIle	/alSerAspPheLeuLe	aLeuValGlnGlyV	LeuLeuAl	1	ş
	572)	ж АВТ23207 (1-2572)	US-10-649-273-2_COPY_176_414 (1-239)	-2_COPY_1	0-649-273	US-1
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                          The present invention relates to novel 38650, 28472, 5495, 65507, 81588 or 14354 nucleic acid molecules which encode adenosine deaminase, glycoprotease or seven transmembrane domain (7TM) receptor family members.
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                                                                                                                                                                                                                      New 38650, 28472, 5495, 65507, 81588 or 14354 nucleic acid molecules, useful for diagnosing and treating cancer, immune, cardiovascular, hematopoietic, brain, pain, metabolic, liver or platelet disorders, a
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08-NOV-2000; 2000US-0246772P.
15-NOV-2000; 2000US-0249185P.
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of the invention are useful in diagnosing
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6 in claim 1 of the specification"
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IleSerLysGluValGlyGluAlaSerIleLysValProGlnLeuLysMetGluIle

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CC deaminase), 28472 (encoding a glycoprotease), 5495 (encoding a 7) CC transmembrane receptor), 65507, 81580 or 14354 nucleic acid molecule (or CC a sequence which is at least 60% identical to the six nucleic acids or CC their open reading frames, fragments of at least 15 nucleotides or CC their open reading frames, fragments of at least 15 nucleotides or CC with the American Type Culture Collection as Accession No. not defined in CC the specification, which encodes the amino acid sequence). Also included CC are a host cell containing the nucleic acids (used to produce the CC proteins), the encoded proteins, an antibody that selectively binds to CC the polypeptide, and identifying a compound that binds to/modulates the CC activity of the polypeptide. The nucleic acid molecules, polypeptides and CC methods are useful for diagnosing, treating cancer, aberrant cellular CC proliferation and/or differentiation, immune disorders, heart disorders, CC cardiovascular disorders including endothelial cell disorders, pain CC cand metabolic disorders, blood vessel disorders, brain disorders, many CC examples of these disorders are given in the specification). The present CC sequence is the Human CDNA 28472 encoding a glycoprotease
                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated 38650, 28472, 5495, 65507, 81588 and 14354 nucleic acid molecules, useful for diagnosing, treating cancer, pain, or immune, heart, endothelial cell, hematopoeitic, blood vessel, brain, metabolic
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(KAPE/) KAPELLER-LIBERMANN
(GLUC/) GLUCKSMANN M A.
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Cancer; aberrant cell proliferation; aberrant cell differentiation; breast cancer; ovarian cancer; prostate cancer; colon cancer; lung cancer; immune disorder; heart disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1820 BP;
                                                  cDNA encoding novel human glycoprotease 26472
                                                                             30-JAN-2003
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                                                                                                                                                                                                                                    GGCATTITACATGACATAGAAGGCATCCGCTATGAACCAAAATGTCCTCTTGGAGTAGAC 1330
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                                                                                                                                                                                                                                                                                                     CysThrAspAsnGlyIleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeu 200
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                                                                                                                                                                                                                                                                                                                                      GCTCTGGAAATTTTAACAAACGCAACACAGTGCACTTTGTTGTGTCCTCCTCCCAGACTA 1210
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                 Score:
                                                                                                                                                                                                                                                                                     CC The invention describes isolated 38650, 28472, 5495, 65507, 81588 and CC 14354 nucleic acid molecules (I) and their encoded polypeptides (II). The CR 38650 nucleic acid molecule comprises a sequence encoding adenosine CC deaminase. The 28472 nucleic acid molecule comprises a sequence encoding CC a human glycoprotease. The 5495, 65507, 81588 and 14354 comprise CC sequences that encode a human seven transmembrane domain (77M). The CC 38650, 28472, 5495, 65507, 81588 or 14354 nucleic acid and polypeptide sequences are useful for diagnosing, preventing or treating a subject CC with or at risk of developing a disorder, e.g. cancer or aberrant CC cellular proliferation and/or differentiation (e.g. breast, ovarian, CC prostate, colon or lung cancer), immune disorders, heart disorders, cardiovascular disorders, endothelial disorders, hematopoietic disorders, CC liver disorders or platelet disorders, pain and metabolic disorders, sarcoma, leukaemia, Hodgkin's disease, autoimmune disorders include carcinoma, CC sarcoma, leukaemia, Hodgkin's disease, autoimmune disorders, farnetion, ci schaemic heart disease, Crohn's disease, autoimmune disorders, CC hypertension, atheroselerosis, heart failure, myocardial infarction, CC syndrome, Raynaud's disease, aneurysm, cerebral ischaemia, peripheral curronsa, crechexia or diabetes. This sequence encodes the novel human glycoprotease carcinome and content or diabetes. This sequence encodes the novel human glycoprotease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       endothelial disorder; hematopoietic disorder; blood vessel disorder; brain disorder; pain; metabolic disorder; liver disorder; diabetes; platelet disorder; carcinoma; sarcoma; leukaemia; Hodgkin's disease; autoimmune disorder; hypertension; atherosclerosis; heart failure; myocardial infarction; ischaemic heart disease; Crohn's disease; Grave's disease; Kawasaki syndrome; Raynaud's disease; aneurysm; cerebral ischaemia; peripheral neuropathy; Alzheimer's disease;
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08-NOV-2000; 2000US-0246772P.
15-NOV-2000; 2000US-0249185P.
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/product= "Glycoprotease 28472"
/note= "Specifically claimed in
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                                                                                                    Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic; Gene Therapy; human; secretory protein; membrane proteins; cancer; inflammatory disease; osteoporosis; neurological disease; gene; ss.
                    21-MAR-2002;
                                                              EP1293569-A2
                                                                                                                                               Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isogai T, Sugiyama T,
Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polynucleotides encoding full-length polypeptides, e.g. secretory
/or membrane proteins, useful for developing medicines for diseases
ch the gene is involved, or as target molecules for gene therapy.
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                         AlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProProArgLeu 180
                                                                                                                                          HisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuPro 140
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CysThrAspAsnGlyIleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeu 200
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Hio Y, Otsuka K, Nagai K, Irie R,
Otsuka M, Nagahari K, Masuho Y;
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Conservative: Mismatches: Indels:

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US-10-649-273-2\_COPY\_176\_414 (1-239)

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Gaps: ADQ24627

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                                                       The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples and comparing the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is that of a human soft tissue sarcom within the specification per se but was submitted in CD format by the inventor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
   Sequence 2890 BP;
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                                                                                                               WO2003062376-A2
                                                                                                                                                                                                                                                                                           thrombolytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human diagnostic and therapeutic polynucleotide (dithp), SEQ ID No 100
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protein replacement therapy; human; gene; ds.
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31-JUL-2003

Percent Similarity:
Best Local Similarity:

1.4e-103 995.50 87.82% 87.82% 80.28%

Length:
Matches:
Conservative:
Mismatches:
Indels:

Gaps:

Score:

No.:

Sequence 3358 BP;

1105 A;

577 Ç

601 G;

1075

; 0 U;

0 Other

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The invention relates to a novel isolated human diagnostic and C therapeutic polymucleotide (designated dithp). The novel dithp polymucleotide comprises: any of 188 DNA sequences consisting of 195-7798 comprising a naturally occurring polymucleotide sequence at least 90% identical to the dithp polymucleotide; a polymucleotide complementary to the dithp polymucleotide or its polymucleotide which is at least 90% cidentical; or an RNA equivalent of any of the polymucleotide semiconed cantidatetic, immunosuppressive, neuroprotective, noticipenic, antiinflammatory, cerebroprotective, antilipaemic, citatorpic, virucide, hemostatic, anti-HIV, antithyroid, thyromimetic, crombolytic, anticogulant, anotectic, anti-HIV, antithyroid, thyromimetic, crowel DITHP polymucleotides polypeptide, antiparasitic, anti-Composition, anticogulant, anotectic, anti-HIV, antithyroid, thyromimetic, crowel DITHP polymucleotides polypeptide, antiparasitic, anticompolytic, anticogulant, anotectic, vasotropic, and antiulcer. The covel DITHP polymucleotides polypeptide, antiparasitic, anticomposition, and antiulcer. The covel DITHP polymucleotides polypeptide, antiparasitic, anticomposition, polymucleotides polypeptide and antiulcer. The covel DITHP polymucleotides polypeptide, antiparasitic, anticomposition, these diseases include cancers (e.g. adenocarcinoma, leukaemia, melanoma, brain cancer, breast cancer, cervix cancer, bone cancer, liver cancer, lung cancer) or other cell proliferative disorders (e.g. arteriosclerosis, addison's disease, thyroiditis, multiple sclerosis, osteoarthritis, rheumatoid atheroselerosis, orthosis, hepatitis, polycythemia vera, primary thrombosis, hypotiuitarism, hypogonadism, gigantism, goiter) metabolic carborovascular disease, thyroiditis, composition, developmental disorders (e.g. disease, canxiety, schizophrenia), asstroine, Alzheimer's disease, pick's disease, (c.g. hypercholesteroine, developmental disorders (e.g. uters), metabolic connective tissue disorders (e.g. akinesia or multidrug resistance), or fise
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P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human diagnostic and therapeutic polynucleotides and polypeptides, useful for diagnosing, treating or preventing e.g. leukemia, brain cancer, atherosclerosis, AIDS, thyroiditis, infections, obesity, strok
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peralta CH,
Kristnam SR,
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17-JAN-2002; 2002US-0349413P.
17-JAN-2002; 2002US-0349946P.
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DB; ADE31156.
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, Tuason O, Yap PE, Amshey SR, Dam
ta CH, Lewis SA, Chen A, Marwaha R,
nam SR, Kolluru V, Panesar IS;
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m TC, Liu
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Lan RY,
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u TF, Gerstin E
, Urashka ME;
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                                                                                                                                      CAPNS; tryptase 4; sialoglycoprotease; enzyme; genetic disease; neurological; neuropsychological; psychotic illness; transgenic animal;
             05-DEC-2001; 2001WO-US046405
                                                                     WO200245491-A2
                                                                                                 Mus musculus.
                                                                                                                           gene;
                                                                                                                                                                   Murine; mouse; protease; calcium activated neutral protease type 5;
                                                                                                                                                                                               Murine sialoglycoprotease-like gene sequence SEQ ID NO:7.
                                                                                                                                                                                                                              07-NOV-2002
                                                                                                                                                                                                                                                          ABQ75508;
                                                                                                                                                                                                                                                                                     ABQ75508 standard;
                                         13-JUN-2002.
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Sequence 1572 BP;

459 A; 337 C;

340 G; 429

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U; 7 Other;

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Comprising a disruption in a protease target gene (PG) selected from CC calcium activated neutral protease type 5 (CAPN5) gene, tryptase 4 gene CC and sialoglycoprotease-like gene. Also described is a targeting construct (CII), comprising a first polymucleotide sequence homologous to at least a first portion of PG, a second polymucleotide sequence homologous to at least a second portion of PG and a selectable marker. (II) is useful for CC producing a transgenic mouse comprising a disruption in a protease target CC gene, by introducing (II) into a cell, introducing the cell into a CD blastocyst, implanting the resulting blastocyst into a pseudopregnant CC mouse, where the pseudopregnant mouse gives birth to a chimeric mouse, CC and breeding the chimeric mouse to produce the transgenic mouse. (I) is CC useful for identifying an agent that modulates the expression or function CC determining whether the expression or function of the disrupted protease carget gene, by administering an agent to (I) and CC determining whether the expression or function of the disrupted protease carget gene in (I) is modulated. (I) is also useful for testing the CC efficacy of proposed genetic and pharmacological therapies for human CC genetic diseases, such as neurological, neuropsychological or psychotic illness. The present sequence represents murine sialoglycoprotease-like gene sequence, which is used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel transgenic animal, comprising a disruption in protease target gene, is useful for identifying agents that ameliorates a phenotype associated
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06-DEC-2000; 2000US-0251820P.
13-DEC-2000; 2000US-0255971P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present invention describes a non-human transgenic animal (I)
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Percent Similarity:
Best Local Similarity:
Query Match:
DB: S 밁 S 밁 ð 밁 S 밁 S Alignment Scores: Pred. No.: US-10-649-273-2\_COPY\_176\_414 (1-239) 101 588 528 768 708 648 81 61 41 21 1 LeuLeuAlaLeuValGlnGlyValSerAspPheLeuLeuLeuGlyLysSerLeuAspIle GlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCys HisPheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGly AlaProGlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGlu LeuGlnHisValThrAspLysIleIleMetLysLysGluLysGluGluGlyIleGluLys CysSerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPhe CTTCAACATATTACTGATAAGCTAATAACACACACAAGGAAAAAGAAGGCATTGAGAAG CTGTTGGMRTTAGTCCAAGGTGTTTCCGATTTCCTGCTCCTTGGGAAGTCTTTGGACATA TGTTCTACAATGAGTGGTGGAAAAGCTATAGAACAGTTGGCCAAAGACGGAAATAGATTC 1.28e-89 870.00 82.77% 77.31% x ABQ75508 Length: Matches: Mismatches: Indels: Conservative: (1-1572)1572 184 13 37 5

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                      The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 20426; 103pp; English.
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           n; chromosome mapping; gene mapping; gene therapy; forensic;
supplement; medical imaging; diagnostic; genetic disorder; ss.
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are useful for treating disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                DNA up-regulated in
                                             20-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPheHisPhe
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                                                                                                                                                             GACATAGAAGGCATCCGCTATGAACCAAAGTATGTGGCTCCTTCAGGGCTG
                                                                                                                                                                            AspIleGluGlyIleArgTyrGluProLys-----CysProLeuGlyVal 219
                                                                                                                                                                                                                     GGCATTATGAAATGCATGAATGGTATTGAAAGACTACGTGCTGGCTTGGGCATTTTACAT
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                murine multipotent progenitor cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No . :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 371 BP; 104 A; 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Classifying an unknown multi-lineage affiliated gene comprises isolating expressed nucleic acid sequences from the discrete cell sub-populations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene potential; multi-lineage; cell commitment; haematopoietic stem cell; HSC; multipotent-progenitor; MPP; common lymphoid progenitor; CLP; common myeloid progenitor; CMP; bone marrow stem cell; mouse; murine; ds.
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GCATGGAATGGAATTGAANGATTACGTGCNGNCTTNGGCNTTNTACNTGANNTAGAAGAC
                   ÄlafrpÄsnGiylieGiuArgLeuArgAlaGlyLeuGlyIleLeuHisAspIleGluGly 208
|||||||||||||||||
                                                                                      ThrGlnCysThrLeuLeuCysProProProArgLeuCysThrAspAsnGlyIleMetIle 188
                                                                                                                                    TCTGGAGGTGTTGCAAGTAACTTGTACATCCGAAAAGCATTGGAAATTGTCGCAAATGCA
                                                                                                                                                          SerGlyGlyValAlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAla 168
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AspIleAlaAlaThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArg

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                                                                                                                                                                                                                                                                                                  CC This invention relates to a novel method for predicting gene potential by CC associating nucleic acid sequences of unknown function with particular CC sub-population profiles. Specifically, it refers to classifying an CC unknown multi-lineage affiliated gene by collecting hybridisation data to develop a gene expression map, in order to determine the discrete sub-CC population where it is expressed. The present invention describes methods CC population where it is expressed. The present invention describes methods CC renewing haematopoietic (blood) stem cells (HSCs), as well as the non-CC self renewing multipotent progenitors (MPPs), common lymphoid progenitors (CLPs) and common myeloid progenitors (CMPs), which are collectively CC referred to as bone marrow stem cells populations. As such, these methods CC can be used to identify associated multi-lineage affiliated genes and CC hence the underlying molecular mechanisms in physiological haematopoietic CC development. This polynucleotide sequence is DNA associated with a murine CC MPP sub population of cells of the invention.
                                                                                                                                                                                                                                                  Sequence 371
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Search completed: February 16, 2005, 13:59:01 Job time: 468.139 secs

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-Q=(cgn2 1)USPTO, Spool)US10649273/runat 14022005 114704 16425/app query.fasta_1.1429
-DB=Issued Patents NA -QFMY=fastap -SUPFIX=rni -MINMATCH=0.1 -LOOFCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -MAXIEN=200000000
-LOCAL -OUTFMT=pto -NORM=ext -HBAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10649273 @CGN 1 1 292 @runat 1 4022005 114704 16425 -NCCU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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                US-09-774-528-177
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Sequence 21, Appl
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US-09-710-279-3566	US-08-311-731A-131	US-09-221-017B-794	US-08-781-986A-102	US-08-956-171E-102	US-09-134-000C-1551	US-09-149-624-1	US-09-438-185A-1	US-09-198-452A-1	US-09-107-433-1618	US-09-790-988-1	US-09-692-570-1	US-08-916-421B-1	US-09-328-352-261	US-09-620-312D-6	US-09-583-110-2196	US-09-066-512-1	US-08-961-527-214	US-09-134-001C-1072	US-09-536-784-51	US-08-961-083-51	US-09-103-840A-1	US-09-103-840A-2	US-09-602-777A-147	US-09-710-279-3985	US-09-710-279-727	US-08-987-121A-3	US-08-987-121A-5	US-09-107-532A-2955	US-08-087-797-1	US-09-489-039A-2050	US-09-543-681A-2341	US-09-902-540-503
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## ALIGNMENTS

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US-09-774-528-177
                                                                                         NUMBER OF SEQ ID NOS: 441
SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 177
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 177, Application US/09774528 Patent No. 6743619
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LENGTH: 1416
TYPB: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (205)..(1305)
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CURRENT APPLICATION NUMBER: US/09/774,528
CURRENT FILING DATE: 2001-01-30
                                                                                                                                                                             APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6743619el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
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Zhao, Qing A.
Yang, Yonghong
Xue, Aidong J.
Wehrman, Tom
Wang, Jian-Rui
Wang, Dunrui
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Zhang, Jie
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Sequence 23, Application US/10067443

Patent No. 6642041

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED
TITLE OF INVENTION: SPINAL CORD, MP-1
FILE REFERENCE: D0073 NP
CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT PILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/262,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
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; SEQ ID NO 23
; LENGTH: 1526
; TYPE: DNA
; ORGANISM: homo sapi
US-10-067-443-23
RESULT 3
US-10-067-443-1
; Sequence 1, Application US/10067443
; Patent No. 6642041
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLECTIDE ENCODING
; TITLE OF INVENTION: SPINAL CORD, MP-1
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Query Match:
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; FILE REFERENCE: D0073 NP
; CURRENT APPLICATION NUMBER: US/10/067,443
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/266,518
; PRIOR PILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 60/282,814
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 2197
; TYPE: DNA
; ORGANISM: Homo sapiens
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DB:
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Sequence 21, Application US/10067443

Patent No. 6642041

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
ITILE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOTIFIE OF INVENTION: SPINAL CORD, MP-1

FILE REFERENCE: DO073 NP
CURRENT APPLICATION NUMBER: US/10/067,443

CURRENT FILING DATE: 2002-02-05

PRIOR APPLICATION NUMBER: US 60/266,518

PRIOR APPLICATION NUMBER: US 60/262,814

PRIOR APPLICATION NUMBER: US 60/282,814

PRIOR FILING DATE: 2001-04-10

NUMBER OF SEQ ID NOS: 71
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; TYPE: DNA
; ORGANISM: homo sapiens
US-10-067-443-21
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PheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCys 175
                                   ArgaspleuleuProGlmAsmAsmAlaValleuValAlaSerGlyGlyValAlaSerAsm 155
                                                                                                                            HisThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGln 135
                                                                                                                                                                                                                                                        ATTAGTAAAGTTGAACAGATAAATATTCCTGGATTGTGCCTAAAAATAGCTGCTCATTTC 908
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                                                                                                             CACACAATGGCATGTCATCTTGTGAAAAGAACACATCGGGCTATTCTGTTTTGTAAGCAG
                                                                                                                                                                                                    ------GluLysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGln 115
                                                                                                                                                                                                                                                                                                                                CTTCAACACGTTACTGATAAAATAATAATGAAAAAGGAAAAAGGAAAGGTATATTTCTA 848
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151 yValAlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCy	SAAGGGCAAAT 12139 1CysHisLeuVa 123	12080 ATTCCTGGATTGTGCCTAAAAATAGCTGCTCATTTCTGCAGGTATTGAGAAGGGGCAAAT 103 eLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCysHisLeuVa	, & B
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GGGATAGTTTATTATTGTTTAATGCTGATATTTTTCTCCAGGTTTA	BAACAGATAAAT 12079	12020 ATAATGAAAAAGGAAAAAGGAAGGAAGGTATATTTCTAATTAGTAAAGTTGAACAGATAAAT	문 4
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146	[hrAspLysIle 88	69 HisHisAlaLysAsnCysAspPheSerPheThrGlyLeuGlnHisValThrAspLysIle	S
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12860 ATATCAAAGAATAATTTTTTCAGAGTTATGTAGTAAAATGCACAAAATAATAAAAATTTC	54)	.39) x US-10-067-443-2	ũ
146		58.47% Indels:	Query DB:
12800 TATAAACTAAAGTGGGAAAATGTTTAAATGGTAGTAATTCATAGATGGAATTTTACATGG		t Similarity: 32.86% Conservative: ccal Similarity: 32.86% Mismatches:	m M
146		No.: 3.21e-86	Pred.
12740 CTTAAAAGCCTTGACAAACATCCTGTTTAACTGTATCTTAAACTTTATTCATTTAAAAAT		C CC THAT PROTEINS	<u> </u>
146		; ORGANISM: homo sapiens IIS-10-067.443-20	<del></del>
12680 AATGTTGATAAAGTTCTGATAATCCACTATATTGTACCAGCCAAAAATCCCTTTAATTGTG		TYPE: NA	
146		SOFTWARE: PatentIn version 3.0	
12620 TTTTTAATAAGCCAGTCAAATTTAGCAGTGGGAGGTGGTATTCCAACTTTCGTGACACT		PRIOR FILLING DATE: 2001-04-10 NIMBER OF SEC ID NOS: 71	
146		PRIOR FILING DATE: 2001-02-05 PRIOR FILING DATE: 2001-02-05	
12560 ATTTTTAGAAAAATAGGTGGATTTCCTTCATCCTTTGATGAAATCCCTTTGTTTG		CURRENT AFFLICATION NUMBER: US/10/06/,443 CURRENT FILING DATE: 2002-02-05 DRIOR-ADDITCATION NUMBER- US 60/266 518	
146		FILE REFERENCE: DO073 NEWS 100 / NE 1	
12500 CTTGTTGGATTTAAAAGAGGGCTTACAATAAAGAAAGTAAATGCAGTAACTGCTATCACT	A NOVEL METALOPROTEASE HIGHLY EXPRESSED I	TITLE OF INVENTION: SPINAL CORD. MP-1 TITLE OF INVENTION: SPINAL CORD. MP-1	
146		ADDITONY Reject.	
12440 TGGTAGCTTTATGGGACAGCTGTATAGCTTCTATGGCACATAAGTCTAATTTTGCATCTT		Parent No. 6642041	، و
146		RESULT 5	문문
12380 CCCTGACAGTATGAAATTATGCAGGATAGGAAAGACTAACAGCCATTTCTTGTACTAGTT		1329 AAAATGGAGATA 1340	밁
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146	AlProGlnLeu 235	216 ProLeuGlyValAspIleSerLysGluValGlyGluAlaSerIleLysValProGlnLeu	Ş
143 nAlaValLeu		196 LeuArgAlaGlyLeuGlyIleLeuHisAspIleGluGlyIleArgTyrGluProLysCys         209 CTACGTGGTGGCTTGGGCATTTTACATGACATAGAAGGCATCCGCTATGAACCAAAATGT	ት
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LENGTH: 94750
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CURRENT APPLICATION NUMBER: US/09/596,002
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: 60/140,121
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PERL Program
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NAME/KEY: misc_feature
OTHER INFORMATION: Incy
PUBLICATION INFORMATION:
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ORGANISM: M. catarrhalis
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24464 GCCTATGAGCTGCCAAGACCCATGCAGCAT---AAAGGGCTGGATTTTTCGTTCAGTGGC 24520
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                           HisPheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGly 80
                                                                              CysSerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPhe
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TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARI
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709.2005-001
CURRENT PILICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 806
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Patent No. 6673910
GENERAL INFORMATION:
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TYPE: DNA
ORGANISM: M.catarrhalis
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                                                                                                                                   AlaProGlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGlu 40
                                            CysSerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPhe 60
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GTGGTCCAAATATCGAAAAATTAGCCAAAAAACGGCAACCCACAC 603
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                                                                                                                                                                                                                                                          APPLICATION INCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REPERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-07-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 884

LENGTH: 1059

TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 884, Application US/09252991A Patent No. 6551795
GENERAL INFORMATION:
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   ProGlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGluCys 41
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                                                   LeuAlaLeuValGlnGlyValSerAspPheLeuLeuLeuGlyLysSerLeuAspIleAla 21
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Matches:
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                                                                                                                                                   Alignment Scores: Pred. No.:
                                                                                                                                                                                                US-09-252-991A-801
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                                                                                                                                                                                                                                        SEQ ID NO 801
LENGTH: 1206
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                                                                                                                                                                                                                            TYPE: DNA
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US-10-649-273-2_COPY_176_414 (1-239) x US-09-252-991A-801 (1-1206)
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Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                           ORGANISM: Pseudomonas aeruginosa
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                                                                                                                           Conservative: Mismatches: Indels:
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Matches:
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RESULY 17

US-09-557-884-1/c
; Sequence 1, Application US/09557884
; Patent No. 6506581
; PATENT INFORMATION:
; APPLICANT: Fleischmann et al.
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd
            ZIP: 20850

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch diskette

COMPUTER: Dell Pentium

OPERATING SYSTEM: MS DOS v6.22

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/557,884

FILING DATE: 25-Apr-2000

CLASSIFICATION: «Uncown»

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

TILING DATE: JUN-5-1995

FILING DATE: JUN-5-1995

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1141 ---CAGCATGACGGCCCGGCGATCAGCGTCCAGCCGCCTGGCCGATG 1185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102 GlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCysHis 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      823 AAGACCTTTÁCCCTGAAC---ACCTGGCAGCGTTGCGTCGÁGGCCGGCGACGACAGCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             763 TTCGTGTTCCCGCGGCCGATGACCGATCGCCCCGGCCTGGACTTCAGCTTCAGCGGGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IleLeuHisAspIleGluGlyIleArgTyrGluProLysCysProLeu 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGlyLeu 81
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STATE: MD
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NAME: Michelle S. Marks
                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
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Best Local Similarity:
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                                                                                         Sequence 1, Application US/09643990A Patent No. 6528289
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            552791 TTAGTGCGTGTCGATGGTGTAGGAAAATATGAAGTGATAGGAGAATCTATTGATGATGCT 552732
                                                                                                                                                                                                                                                                                                                                   552371 GAAACGCTTGCGCACTTAATGCAAAATTTAGGTGGCGAAGTGTTTTATCCTCAACCTCAA 552312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               552467 GATACTCTTGCC---
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LENGTH: 1830121 base pa
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ II
                 APPLICANT: Robert D. Fleischmann
Mark D. Adams
Owen White
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GAAACAGGCTATAAACGTTTAGTGATTGCGGGAGGGGTGAGCGCAAATAAAAAACTCCGA
                                                                                                                                                                                                                                   TTTTGTACAGATAATGGTGCGATGATTGCTTACACAGGTTTTTTTACGTTTAAAAACAAGGT
                                                                                                                                                                                                                                                              LeuCysThrAspAsnGlyIleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGly 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CysHisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeu 139
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Hamilton O. Smith
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Matches:
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Query Match:
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APPLICATION NUMBER: 08/487,429

PILING DATE: 1995-06-07

APPLICATION NUMBER: 08/426,787

PILING DATE: 1995-04-21

ATTORNEY/ACENT INFORMATION:

NAME: Kenley K. HOOVET

REGISTRATION NUMBER: 40,302

REFERENCE/DOCKET NUMBER: PE186P1C1

TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskett
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
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LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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APPLICATION NUMBER: US/09/643,990A
FILING DATE: 23-Aug-2000
CLASSIFICATION: <Unknown>
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TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
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LysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAla 119
                                           AAAACATTTGCCGCAAATACAGTTAATCAAGCAATTAAAAACGAGGGCGAACTGATAGAG
                                                                                                                             TICACATTICCACGICCAATGACAGATCGIGCAGGCCITGATTITAGITITTCTGGITIA 552573
                                                                                                                                                                                                                                               SerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPheHis
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                                                                                   GlnHisValThrAspLysIleIleMetLysLysGluLysGluGluGly-----IleGlu
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
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TYPE: DNA
ORGANISM: Myxococcus xanthus
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101 GlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCys 120
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                                                                                               LeuGlnHisValThrAspLysIleIleMetLysLysGluLysGluGluGlyIleGluLys 100
                                                                                                                                                                           HisPheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGly
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SEQ ID NO 503
LENGTH: 2582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: 18/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
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                                                                                                   81 LeuGlnHisValThrAspLysIleIleMetLysLysGluLysGluGluGlyIleGluLys 100
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                               GlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCys 120
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GGGCAGGCGCTG-----GCGGATTTGTGCGCGTCCTTCCAGGAGGCCGTGGCGGAC 794
                                                                     TTGAAG------ACGGCGGTGCTGCACCACGTGCAGAAGCACGGCGTGCCGCAG
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FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 2341
LENGTH: 1074
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2341, Application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: GARY BRETON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Proteus mirabilis
                                    122
                                                                                                                                                                 102
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LeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuProGln 141
                                                                                                                                                        GlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCysHis 121
                                                                                                                                                                                                                                                                                        GlnHisValThrAspLysIleIleMetLysLysGluLysGluGluGlyIleGluLysGly 101
                                                                                                                                                                                                                                                                                                                                                              TTTGTTTTTCCTCGTCCCATGACAGACAGACCCGGACTCGACTTTAGTTTCTCTGGTTTA
                                                                                                                                                                                                                                                                                                                                                                                            PheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGlyLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPheHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTGGTGAAGCATTTGATAAAACAGCCAAGCTATTGGGGGCTT---GATTATCCC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CysThrAspAsnGlyIleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----GGCCACAAGCAGTTGGTGCTGTGCGGGGCGTCGCCGGAACTCGCGGCTGCGGGCA
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                                                                                               -- CAAACTCGAGCAGATATTGCGCGTGCTTTTGAAGATGCCGTAGTAGATACT
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212.00
44.95%
30.28%
17.10%
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₹ ¥	790 TTGGCAATAAAATGTCGTCGAGCATTAGAGCAA 822 142 AsnAsnAlaValLeuValAlaSerGlyGlyValAlaSerAsnPheTyrIleArgArg 160
Ъ	823 ACAGGCTTTAAACGCTTAGTGATGGCTGGGGGCGTAAGTGCTAACCGTACTTTACGCGCC 882
¥	.euGluIleLeuThrAsnAlaThrGlnCysThrLe :: :::::
ř	Ä:
ਝ ਝ	181 CY8ThrAspAsnGlyIleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeu 200 
Ϋ́	leArgTyrGluProLy
8	1003 GAGGGCCTTTAGGGTGACAGTGAGACCACGTTGGCCTTTA 1044
JS-09-489-039/ JS-09-489-039/ JS-09-489-039/ JS-09-489-039/ JS-09-489-039/ JS-09-489-039/	UULT 15 09-489-039A-2050 09-489-039A-2050 iequence 2050, Application US/09489039A iequence 2050, Application US/09489039A iatent No. 6610836 iatent No. 6610836 iatent No. 6610836 iatent No. 6610836 iatent No. 6610836 iatent No. 6610836 iatent No. 6610836 iatent No. 6610836 iatent No. 6610836 iatent No. 6610836 iatent No. 6610836 iatent No. 6610836 iatent Of Invention: NUCLEIC ACID AMD AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS FILER REFERENCE: 2709.2004001 CURRENT APPLICATION NUMBER: US/09/489,039A CURRENT FILING DATE: 2000-01-27 PRIOR APPLICATION NUMBER: US 60/117,747 PRIOR PILING DATE: 1999-01-29 INVERSOR OF SEQ ID NOS: 14342 ieq ID NO 2050 LENGTH: 1032 TYDE: DNA ORGANISM: Klebsiella pneumoniae 09-489-039A-2050
Pred. No. Score: Score: Sercent Sercent Sest Loca Query Mat	nment Scores:  . No.:  1.55e-17  Length:  205.00  Matches:  66  ent Similarity:  43.58%  Conservative:  29  Local Similarity:  30.28%  Mismatches:  93  Local Similarity:  16.53%  Indels:  30  Gaps:  7
JS-10-649-	3-273-2_COPY_176_414 (1-239) x US-09-489-039A-2050 (1-1032)
ਲ ਝ	2 LeuAlaLeuValGlnGlyValSerAspPheLeuLeuLeuGlyLysSerLeuAspIleAla 21
<b>ਲ</b> ਝ	22 ProGlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGluCys 41
ਲ ਝ	42 SerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPheHis 61        553GCGGGCCGATGCTGTCGAAAATGGCGTCCCAGGGCACGCCGAAGGCCGC 600
ਲ ਕ	62 PheAspIleLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGlyLeu 81
ਰ ਝ	82 GlnHi8ValThrAspLy8IleIleMetLy8Ly8GluLy8GluGlyIleGluLy8Gly 101 ::: 661 AAGACCTTCGCCGCCAACACCATTCGCAGCAACGGCGATGAG 705
ਲੋਂ ਝੋਂ	102 GlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCysHis 121 :::            706CAAACCCGCGCCGACATCGCCCGGGCGTTGAGGATGCGGTCGATACG 756
¥	122 LeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuProGln 141

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142 ABNABN---AlaValLeuValAlaSerGlyGlyValAlaSerABNPheTyrIleArgArg 160
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790 ACCGGCTTTAAGCGTCTGGTGATGGCGGGAGGCGTTAAGCGCTACCCTGCGGGCG 849
                                                               161 AlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProArgLeu 180
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Search completed: February 16, 2005, 22:38:34 Job time : 1516.1 secs

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-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
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-FGAPEOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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/cgn2_6/ptodata/2/pubpna/US09E_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIBS

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US-10-282-122A-31809 US-09-815-242-6207 US-10-282-122A-20511 US-10-425-114-28614	5-242-9682 82-122A-3930 82-122A-3225 82-122A-4197 82-122A-1972 37-963-9137		100-100-100-100-100-100-100-100-100-100	649-273- 651-722- 012-140- 012-749- 723-860- 067-443- 669-273- 651-722-	-10-120-98 -10-067-44 -10-669-27 -10-651-72 -10-651-72 -10-649-27 -10-651-72
Sequence 31809, A Sequence 6207, Ap Sequence 20511, A Sequence 28614, A	quence 9682, equence 393(equence 322) equence 4191 equence 1922 equence 1923	Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence	Sequence 3119, Ap Sequence 66417, A Sequence 11249, A Sequence 11674, A Sequence 50, Appl Sequence 26972, A Sequence 38, Appl	2200	177, 23, 23, 23, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,

## ALIGNMENTS

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RESULT 1

US-10-120-988-177

Sequence 177, Application US/10120988

Publication No. US20030219745A1

GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Hang, Dunrui
APPLICANT: Wang, Dunrui
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20030219745A1el Nucleic Acids and TITLE OF INVENTION: Polypeptides

FILE REFERENCES: 802CON
CURRENT APPLICATION NUMBER: US/10/120,988

CURRENT PILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: 09/774,528
PRIOR FILING DATE: 2001-01-30

NUMBER OF SEQ ID NOS: 441

SOFTWARE: pt_FL_genes Version 2.0
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NO 177

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; LENGTH: 1416
; TYPB: DNA
; ORGANISM: Homo sapiens
; PEATURE:
; NAME/KEY: CDS
; LOCATION: (205)..(1305)
US-10-120-988-177
US-10-067-443-23
Sequence 23, Application US/10067443
; Publication No. US20030082782A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
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CURRENT APPLICATION NUMBER: US/10/067,443
CURRENT FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR PILING DATE: 2001-04-05
PRIOR PILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.0
SEQ ID NO 23
LENGTH: 1526
TYPE: DNA
ORGANISM: homo sapiens
US-10-067-443-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING TITLE OF INVENTION: SPINAL CORD, MP-1 FILE REFERENCE: D0073 NP
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                                     CysThrAspAsnGlyIleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeu
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APPLICANT: BRISTOI-Myers Squibb Company
TITLE OF INVENTION: POLYNCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
FILE REFERENCE: D0073 CNT
CURRENT APPLICATION NUMBER: US/10/649,273
CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/67,443
PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PRICH TONS: 71
SOFTWARE: PATENTIAL VERSION 3.2
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Query Match:
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; ORGANISM: homo sapiens
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; ORGANISM: homo
US-10-651-722-23
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CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
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Publication No. US20040048302A1
GENERAL INFORMATION:
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SEQ ID NO 23
LENTH: 1526
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TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
FILE REFERENCE: D0073 DIV
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HisteuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuPro 140
                                                                                                                                                                                                                                                                                                          AlaProGlyAspMetLeuAspLysValAlaArgArgLeuSerLeuIleLysHisProGlu 40
                                                                        GlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCys
                                                                                                                               LeuGlnHisValThrAspLysIleIleMetLysLysGluLysGluGluGlyIleGluLys
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Sequence 1, Application US/10067443

Publication No. US20030082782A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: SPINAL CORD, MP-1

FILE OF INVENTION: SPINAL CORD, MP-1

FILE REFERENCE: D0073 NP

CURRENT APPLICATION NUMBER: US/10/067,443

CURRENT FILING DATE: 2002-02-05

PRIOR APPLICATION NUMBER: US 60/266,518

PRIOR APPLICATION NUMBER: US 60/266,518

PRIOR FILING DATE: 2001-02-05

PRIOR APPLICATION NUMBER: US 60/262,814

PRIOR FILING DATE: 2001-04-10

NUMBER OF SEQ ID NOS: 71

SOFTWARE: PatentIn version 3.0

SEQ ID NO 1

LENGTH: 2197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA;
; ORGANISM: Homo sapiens;
; FEATURE:
; NAME/KEY: CDS;
; LOCATION: (231)..(1472)
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LeuGlnHisValThrAspLysIleIleMetLysLysGluLysGluGluGlyIleGluLys 100
                                    TGCTCCACCATGAGTGGTGGGAAAGCCATAGAACATTTGGCCCAAACAAGGAAATAGATTT
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GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
PILE REPERENCE: D0073 CNT
CURRENT APPLICATION NUMBER: US/10/649,273
CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US 60/66,518
PRIOR FILING DATE: 2001-02-05
PRIOR PILING DATE: 2001-02-05
PRIOR PILING DATE: 2002-02-05
PRIOR PILING DATE: 2002-02-05
PRIOR PILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.2
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Publication No. US20040043407A1
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: (23
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                                 IleSerLysGluValGlyGluAlaSerIleLysValProGlnLeuLysMetGluIle 239
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CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR PILING DATE: 2002-02-05
PRIOR PILING DATE: 2002-04-10
PRIOR FILING DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.2
SEQ ID NO 1
LENGTH: 2197
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Publication No. US20040048302A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1

FILE REFERENCE: D0073 DIV

CURRENT APPLICATION NUMBER: US/10/651,722
                                                                                        FEATURE:
NAME/KEY: CDS
LOCATION: (231)..(1472)
                                                                                                                                              ORGANISM: Homo
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         Sequence 21, Application US/10067443

Publication No. US20030082782A1

Publication No. US20030082782A1

PERRAL INFORMATION: SCHOOL Company

TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE HIGHLY EXPRESSED

TITLE OF INVENTION: SPINAL CORD, MP-1

PILE REFERENCE: D0073 NP

CURRENT APPLICATION NUMBER: US/10/067,443

CURRENT FILING DATE: 2002-02-05

PRIOR PPLICATION NUMBER: US 60/266,518

PRIOR PPLICATION NUMBER: US 60/262,914

PRIOR PILING DATE: 2001-02-05

PRIOR APPLICATION NUMBER: US 60/262,914

PRIOR PILING DATE: 2001-04-10

NUMBER OF SEQ ID NOS: 71

SOFTWARE: Patentin version 3.0
 SEQ ID
 NO 21
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Percent Similarity:
Best Local Similarity:
Query Match:
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; SEQ ID NO 21
; LENGTH: 1387
; TYPE: DNA
; ORGANISM: homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE,
FILE REFERENCE: D0073 CNT
CURRENT APPLICATION NUMBER: US/10/649,273
CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR PILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
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ProProProArgLeuCysThrAspAsnGlyIleMetIleAlaTrpAsnGlyIleGluArg 195
                                                                                                                        ArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyValAlaSerAsn 155
                                                                                                                                                                                                                                                                                                              ATTAGTAAAGTTGAACAGATAAATATTCCTGGATTGTGCCTAAAAATAGCTGCTCATTTC
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                                     TICTATATCCGCAGAGCTCTGGAAATTTTAACAAACGCAACACAGTGCACTTTGTTGTGT 1148
                                                     PheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCys 175
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APPLICANT: Bristol-Myers Squibb Company
INTILE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALOPROTEASE, MP-1
FILE REFERENCE: D0073 DIV
CURRENT APPLICATION NUMBER: US/10/651,722
CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US 60/266,518
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 10/067,443
PRIOR FILING DATE: 2002-02-05
PRIOR APPLICATION NUMBER: US 60/282,814
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 71
SOPTWARE: PatentIn version 3.2
SOPTWARE: PatentIn version 3.2
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; TYPE: DNA
; ORGANISM: homo s
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Best Local Similarity:
Query Match:
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Matches:
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Sequence 6, Application US/10012140

Publication No. US2003009017A1

GENERAL INFORMATION:

APPLICANT: Kelby, Kevin R.

APPLICANT: Kapeller-Libermann, Rosana

APPLICANT: Kapeller-Libermann, Rosana

APPLICANT: Glucksmann, Maria A.

TITLE OF INVENTION: 18354 METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND USES

TITLE OF INVENTION: THEREOF

FILLE OF INVENTION: THEREOF

FILLE AFFERENCE: 381552004990

CURRENT APPLICATION NUMBER: US/10/012,140

CURRENT APPLICATION NUMBER: 60/246,768

PRIOR APPLICATION NUMBER: 60/246,772

PRIOR FILLING DATE: 2000-11-08

PRIOR APPLICATION NUMBER: 60/246,772

PRIOR APPLICATION NUMBER: 60/246,772

PRIOR FILLING DATE: 2000-11-08

PRIOR APPLICATION NUMBER: 60/249,185

PRIOR APPLICATION NUMBER: 60/249,185

PRIOR FILLING DATE: 2000-11-15

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
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                                                              US-10-649-273-2_COPY_176_414 (1-239) x US-10-012-140-6 (1-1245)
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LENGTH: 1245
TYPE: DNA
ORGANISM: Homo 6
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                   LeuLeuAlaLeuValGlnGlyValSerAspPheLeuLeuCeuGlyLysSerLeuAspIle 20
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Mismatches:
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APPLICANT: Leiby, Kevin R.

APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Glucksmann, Maria A.

TITLE OF INVENTION: 38650, 28472, 5495, 65507, 81588, AND
TITLE OF INVENTION: 14354 METHODS AND COMPOSITIONS OF HUMAN PROFILE OF INVENTION: THEREOF
FILE REFERENCE: 381552004900
CURRENT APPLICATION NUMBER: US/10/012,140
CURRENT APPLICATION NUMBER: 60/246,768
PRIOR APPLICATION NUMBER: 60/246,772
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/246,772
PRIOR PILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/249,185
PRIOR APPLICATION NUMBER: 60/249,185
PRIOR PILING DATE: 2000-11-15
PRIOR FILING DATE: 2000-11-15
PRIOR FILING DATE: 2000-11-15
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US-10-012-140-4
                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/10012140 Publication No. US20030009017A1 GENERAL INFORMATION:
                                                                 NUMBER OF SEQ ID NOS: 49
SOFTWARE: FRATSEQ for Windows
SEQ ID NO 4
LENGTH: 1820
                     ORGANISM: Homo sapiens FEATURE:
                                                       TYPE: DNA
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RESULT 13
US-10-094-749-400
US-10-094-749-400
; Sequence 400, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
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PRATIONE:
NAME/KEY: misc_feat:
LOCATION: (1)...(188
OTHER INFORMATION: 1
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WAKAMATSU, AI SATO, HIROYUKI

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 400
; LENGTH: 2208
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-094-749-400
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APPLICANT: NASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-14
NUMBER: OF SEQ. ID NOS: 3381
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GlnAsnAsnAlaYalieuWalAlaSerGlyGlyValAlaSerAsnPheTyrIleArgArg
                                                                                                                GlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCys
                                                                                                                                                                                             LeuGlnHisValThrAspLysIleIleMetLysLysGluLysGluGluGlyIleGluLys 100
                                                                                                                                                                                                                                                                                                              CysSerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPhe 60
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NAGAI, KEIICHI
IRIE, RYOTARO
TAMECHIKA, ICHIRO
SEKI, NAOHIKO
YOSHIKANA, TSUTOMU
OTSUKA, MOTOYUKI
                                                         HisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuPro
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                                                                                                                                                                          CTTCAACACGTTACTGATAAAATAATAATGAAAAAGGAAAAAGGGAAGGTATTGAGAAG
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; OTHER INFORMATION: n is
US-10-723-860-7447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.2 SEQ ID NO 7447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Co
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma
FILE REFERENCE: 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT APPLICATION NUMBER: 50/429,739
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 8393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 2890
TYPE: DNA
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LeuGlnHisValThrAspLysIleIleMetLysLysGluLysGluGluGlyIleGluLys 100
                                                            HisPheAspI1eLysProProLeuHisHisAlaLysAsnCysAspPheSerPheThrGly
                                                                                                                         CybSerThrMetSerGlyGlyLybAlaIleGluHisLeuAlaLysGlnGlyAsnArgPhe
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	69 HISHIBALALYBABNCYBASPPRESERPRETNYGLYLEUGINHIBVAITNYASPLYSIIE 88	GCCHINGANCHILIGGCCAMACHAGGARIAGAHILICAIIIIGACAICAMACCICCCIIG II959			1	0	39) x US-10-067-443-20 (1-14364)	58.47% Indels: 380	e: 0.7	8.93e-83 Length: 14364 725.00 Matches: 186		ORGANISM: homo sapiens		on 3.0			02-05 \$ 60/266,518		TITLE OF INVENTION: POLYNUCLECTIDE ENCOYING A NOVEL METALOPROTEASE HIGHLY EXPRESSED I	Dany	pplication US/10067443 . US20030082782A1	443-20	2170	221 IleSerLysGluValGlyGluAlaSerIleLysValProGlnLeuLysMetGluIle 239 (	2113	201 GlyIleLeuHisAspIleGluGlyIleArgTyrGluProLysCysProLeuGlyValAsp 220	181 CysThrAspAsnGlyIleMetIleAlaTrpAsnGlyIleGluArgLeuArgAlaGlyLeu 200 (	161 AlaleuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProProArgLeu 180 (	CAAAATAATGCAGTACTGGTTGCATCTGGTGGTGTCGCAAGTAACTTCTGTATCCGCAGA 2005	160	121 HisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuPro 140 Qy
Qy 146 146	Db 13040 TTTTTCTTTCCAAATTTTTATTACATAGATATGTCATCTGCCCATTACCCCATCTCAAAAT 13099	Qy 146 146	Db 12980 TGGAAGAAAATATACAAAAATGCTAGTAATGTTTGTATGCTATTAGAATTATTAGTAATT 13039	Qy 146 146	Db 12920 AGGGTCTAAAATAGTGTACTATGATTGAAATTATATTAAATAATATTTAGATGAAAGGT 12979	Qy 146 146	Db 12860 ATATCAAAGAATAATTTTTTCAGAGTTATGTAAAATGCACAAAATAATAAAAATTTC 12919	Qy 146 146	Db 12800 TATAAACTAAAGTGGGAAAATGTTTAAATGGTAGTAATTCATAGATGGAATTTTACATGG 12859	Qy 146 146	Db 12740 CTTAAAAGCCTTGACAAACATCCTGTTTAACTGTATCTTAAACTTTATTCATTTAAAAAT 12799	Qy 146 146	Db 12680 AATGTTGATAAAGTTCTGATAATCCACTATATTGTACCAGCCAAAATCCCTTTAATTGTG 12739	Qy 146 146	Db 12620 TTTTTTAATAAGCCAGTCAAATTTAGCAGTGGGAGGTGGTATTCCAACTTTCGTGACACT 12679	Qy 146 146	Db 12560 ATTTTTAGAAAAATAGGTGGATTTCCTTCATCCTTTGATGAAATCCCTTTGTTTG	Qy 146 146	Db 12500 CTTGTTGGATTTAAAAGAGGGCTTACAATAAAGAAAGTAAATGCAGTAACTGCTATCACT 12559	Qy 146 146	Db 12440 TGGTAGCTTTATGGGACAGCTGTATAGCTTCTATGGCACATAAGTCTAATTTTGCATCTT 12499	Qy 146 146	Db 12380 CCCTGACAGTATGAAATTATGCAGGATAGGAAAGACTAACAGCCATTTCTTGTACTAGTT 12439	Qy 146 146	Db 12320 TITTTTCCCAAGACCTTGACCTTGTGTTTAGGATGAACAGATCTTTATGCCTTATGCTAG 12379	Qy 146 146	Qy 143 nAlaValleu 146               Db 12260 TGCAGTACTGGTAAGTTTTATCTCATTTTATAGTAATAGTTACACTTTGCAATATGTTAC 12319	Qy 123 lysargThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnAs 143	CCTGTCTTCAGCAGCAGACATTGCTGCCACAGTACAGCACACAATGGCATGTCATCTTGT	Qy 103 eLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCysHisLeuVa 123	Qy 97

	13520 GCTATGAACCAAAG 13533		₽
	rgTyrGluProLys 214	210	S
13519	13460 GGAATGGTATTGAAAGACTACGTGCTGGCTTGGGCATTTTACATGACATAGAAGGCATCC 13519		фa
210	AsnGlyIleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAspIleGluGlyIleA		Ş
13459	13400 ACTAAGCCTTCCTTCCAGATCTTGGAGCTATTGATTTATTT		뫄
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13399	13340 AGCCACAGGATATACGTGCTTCACTCATAACTATGTAAATATTAATTGCCATTTTATCAT 13399		dα
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13339	CACTTTGTTGTGTCCTCCCAGACTATGCACTGATAATGGCATTATGATTGCATGGTA 13339	13280	90
190	sThrLeuLeuCysProProProArgLeuCysThrAspAsnGlyIleMetIleAlaTrp	171	Ş
13279	TGTCGCAAGTAACTTCTATATCCGCAGAGCTCTGGAAATTTTAACAAACGCAACACAGTG 13279	13220	ф
171	. yValAlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCy	151	<b>ક</b>
13219	13160 TCATATCCATATATGATAGTTATTTTGGTTTTCTCAATTCCTTCAGGTTGCATCTGGTGG 13219		qq
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13159	13100. GGGATAGTTTATTATTGTTTAATGCTGATATTTTTCTCCAGGTTTAATTAGCAGCTTGGT 13159		٩٥ ً -

Search completed: February 17, 2005, 01:27:31 Job time: 500 secs

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Run on:
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February 16, 2005, 12:38:06 ; Search time 10.9109 Seconds (without alignments) 2107.605 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Title: Perfect score: US-10-649-273-2\_COPY\_176\_414 1240

1 LLALVQGVSDFLLLGKSLDI......DISKEVGEASIKVPQLKMEI 239

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

pIR\_79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

9 193.5 15.6	8 195 15.7	7 195 15.7	6 195.5 15.8	5 195.5 15.8	4 199 16.0	3 200 16.1	2 201 16.2	1 201.5 16.2	16.3	9 204.5 16.5	8 205.5 16.6	7 206 16.6	6 209 16.9	209 16.9	209 16.9.	16.9	210.5 17.0	213 17.2	5 17.9	224 18.1	'n	o	6 237.5 19.2	19.2	'n	19.7	19.7	1 326 26.3	Result Query No. Score Match Length
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RESULT 2
AB3902
O-sialoglycoprotein endopeptidase gcp [imported] - Agrobacterium tumefaciens (strain C58, C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 18-Nov-2002

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174.5 174.5 174.5	180 180 179 178	186 183 182	192 189 188.5 186.5	193 192
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344 344 374	3446	33836	346 346 444	348 346
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o-sialoglycoprotei O-sialoglycoprotei probable O-sialogl	o-staloglycoprotes o-staloglycoprotes glycoprotein endop O-staloglycoprotei	glycoproteinase fa glycoprotein endop probable o-sialogl	sialoglycoproteina O-sialoglycoprotei glycoprotein endop probable o-sialogl	sialoglycoproteina sialoglycoproteina

## ALIGNMENTS

Db 433	Оу 225	Qy 181 Db 383	Qy 121 Db 326	Qy 61 Db 276	Qy 1 Db 221	Query Match Best Local Similarity Matches 82; Conser	RESULT 1  E84988  probable O-sialoglycoprot C;Species: Arabidopsis th C;Date: 02-Feb-2001 #sequ C;Accession: E84888  R;Lin, X.; Kaul, S.; Roun M.; Koo, H.; Moffat, K.S. euss, D.; Nierman, W.C.; Nature 402, 761-768, 1999  A;Title: Sequence and ana A;Reference number: A8442  A;Accession: E84888  A;Status: preliminary A;Molecule type: DNA A;Residues: 1-463 <570> A;Residues: 1-463 <570> A;Cross-references: GB:AE C;Genetics: Ac245270  A;Map position: 2 C;Superfamily: O-sialogly
RSEA 436	VGEA 228	CTDNGIMIAWNGIERLRAGLGILHDIEGIRYB	HLVKRTHRAILFCKQRDLLÞQNNAVLVASGGVASNFYIRRALEILTNATQCTLLCÞÞÞRL 180    ::	HFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMAC 120  :  :  :  :   :   :  :  :  :   :   SVKFNVPMKYHKDCNFSYAGLKTQVRLAIEAKBIRNRADIAASFQRVAVL 325	LLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPBCSTNSGGKAIEHLAKQGNRF 60 	h 26.3%; Score 326; DB 2; Length 463; Similarity 33.6%; Pred. No. 4.3e-22; 82; Conservative 34; Mismatches 84; Indels 44; Gaps 5;	RESULT 1  E84888  probable O-sialoglycoprotein endopeptidase [imported] - Arabidopsis thaliana (mouse-ear cress)  C;Species: Arabidopsis thaliana (mouse-ear cress)  C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Jun-2003  C;Accession: E84888  C;Accession: E84888  R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N., Koo, H.; Moifat, K.S.; Cronin, L.A.; Shea, M.; Vankken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999  A;Tille: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197  A;Rocession: E84888  A;Rocession: E84886  A;Rocession: E94886 (STO)  A;Cross-references: GB:AE002093; NID:92583127; PIDN:AAB82636.1; GSPDB:GN00139  C;Gene: At2945270  A;Map postion: 2  C;Superfamily: O-sialoglycoprotein endopeptidase

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C;Accession: AB2902
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, R;Wood, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, I; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Go
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A;Gene: AGR C_4806
A;Map position: circular chromosome
C;Superfamily: O-sialoglycoprotein (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable o-sialoglycoprotein endopeptidase (glycoproteinase) [imported] - Agrobacterium C;Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002 C;Accession: D97677
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                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-366 < KI
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A;Experimental source: strain C58 (Dupont)
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A;Molecule type: DNA
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Matches
                                                                                                                                                                                                                                                                                                                                                                     ;Residues: 1-366 <KUR>
;Cross-references: GB:AE007869; PIDN:AAK88373.1; PID:g15157858; GSPDB:GN00169
                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                 Superfamily: O-sialoglycoprotein endopeptidase;
                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 MACHLVKRTHRAILFCKQRDLLFQNNA--VLVASGGVASNFYIRRALBILTNATQCTLLC 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251 VSRTLKDRIGRGLARFKVE--FPHINGEPALVVAGGVAANQEIRQTLQALCDTHGFRFVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202 FPLPRPMVGEARLDFSFSGLKTAVRQAATAIAPLSEQD-----IADICÁSFQKA
                                                62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 LALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFH
                                                                                                                                         2 LALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-365 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 19.7%; Score 244; DB 2; Similarity 31.9%; Pred. No. 1.1e-14;
                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPPRICTDNGIMIAWNGIERLRAGLGILHDIEGIRYEPKCPLGVDISKE 224
  FPLPRPMVGEARLDFSFSGLKTAVRQAATAIAPLSEQD----
                                             FDIKPPLHHAKNCDFSFTGL----QHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHT 117
                                                                                           LVLVRGVGEYERWGTTIDDALGEAFDKTAKLLGL-PYP-----GGPAVENAAAKGDPDR 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FDIKPPLHHAKNCDFSFTGL----QHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPHRICTDNAAMIAWAGLERMAEG----RQADALEVAPRSRWPLDGSAE 353
                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                     19.7%; Score 244; DB 2;
31.9%; Pred. No. 1.1e-14;
rative 34; Mismatches 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34; Mismatches
                                                                                                                                                                                            92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 365;
                                                                                                                                                                                                                                   Length 366;
                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
  ---IADICASPQKA 251
                                                                                                                                                                                          30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B.; Goldm
Markelz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M.; McClel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Goldman,
ckelz, B.;
                                                                                                                                                                                     C;Accession: E71711
R;Andersson, S.G.B.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Reference number: A71630; MUID:99039499; PMID:9823893
A;Accession: E71711
                                                                                                                                                                                                                                                                                                                       probable o-sialoglycoprotein endopeptidase (gcp) RP037 - Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S
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                                             A; Experimental source: C; Genetics:
                                                                          A;Cross-references: UNIPROT:Q9ZEA8; GB:AJ235270; A;Experimental source: strain Madrid E
                                                                                                                    A; Molecule type: DNA
A; Residues: 1-387 < AND >
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C; Superfamily: O-sialoglycoprotein endopeptidase
                                                                                                                                                             A; Status: preliminary; nucleic acid sequence not shown; translation not
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Matches
                          gcp; RP037
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strain

GB:AJ235269; NID:G3860572; PIDN:CAA14508

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R;Delvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, P.; Mazur, M.; Goltsman, B.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessc Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensi A;Reference number: AD3252; PMID:11756688
A;Accession: AB3274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: I
C;Superfamily: O-sialoglycoprotein endopeptidase
C;Keywords: hydrolase; metalloproteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O-sialoglycoprotein endopeptidase (EC 3.4.24.57) [imported] - Brucella melitensis (strair C;Species: Brucella melitensis C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-359 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: BMEI0175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE008917; PIDN:AAL51357.1; PID:g17982056; GSPDB:GN00190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
304
                                                    176
                                                                                                                     246
                                                                                                                                                                                                                                             198 FALPRPLKGEARLDFSFSGLKTAVRQTATELVPLTDQ---
                                                                                                                                                                                                                                                                                                                                                                        145 MVLVRGIGDYERLGTTIDDALGEAFDKTAKLLGL-PYP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 MACHLVKRTHRAILFCKQRDLLPQNNA--VLVASGGVASNFYIRRALEILINATQCTLLC
                                                                                                                                                                                                                                                                                                           62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69;
                                                                                                                                                                                                                                                                                                                                                                                                                                   2 LALVOGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKOGNRFH 61
                                                    PPPRICTONGIMIAWNGIER 195
                                                                                                                 TMACHLVKRTHRAILFCKQRDLLPQ-NNAVLVASGGVASNFYIRRALBILTNATQCTLLC 175
                                                                                                                                                                                                                                                                                                           FDIKPPLHHAKNCDFSFTGL-----QHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQH 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPHRICTDNAAMIAWAGLERMAEG----RQADALEVAPRSRWPLDGSAB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPPRICTDNGIMIAWNGIBRLRAGLGILHDIBGIRYEPKCPLGVDISKE 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.5%; Score 241.5; DB 2; 34.5%; Pred. No. 1.9e-14; ative 27; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 359;
                                                                                                                                                                                                                                                                                                                                                                        -GGPAVERMALÓGDOKR 197
                                                                                                                                                                                                                                             -----DVTDICASFQA
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R;Stover, C.K.; Pham, X.Q.; Erwin, adman, S.; Yuan, Y.; Brody, L.L.; (.; Lory, S.; Olson, M.V.
                                                                H83572
O-sialoglycoprotein endopeptidase PA0580 [imported] - Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AE005673; NID:gl3421168; PIDN:AAK22058.1; GSPDB:GN00148 C;Genetics:
A;Gene: CC0071
C;Superfamily: O-sialoglycoprotein endopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-367 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolor n. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Reference number: A87249; MUID:21173698; PMID:11259647

A;Accession: F87257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptidase M22 family protein [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001 C;Accession: F87257
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                                                     C;Accession:
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Best Local S
Matches 70
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Matches
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                                                                                                                                                                                                                                         185 GIMIAWNGIERLRAGLGILHDIEGIRYEPKCPL 217
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                                                                                                                                                                                                                                                                                                                                                                                                                            156 VSGVGACKRIGTTIDDAAGEAFDKIAKSIGI-PYP-----GGPALEKLAVGGDPTRYAL 208
                                                                                                                                                                                                                                                                                                                                                                          65 KPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMACHLVK 124
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                                                        1103572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                 RTHRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRALEILTNATQCTLLCPPPRLCTDN 184
                                                                                                                                                                                                                                                                                                                                                                                                                                               VQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PKPIINSGNCNMSFSGLKTAVRTLIMNLKEVNDSV-----INDIAASFOFTIGAILS
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                                                                                                                                                                                                       AAMIALAGAERL--ALGIFDDLDAIA-RPRWPL 347
                                                                                                                                                                                                                                                                             RVDRAMKLYK--DSHDPEDLRFVVAGGVAANGAVRAALLADCEKNGPSPAAPPLAYCTON
                                                                                                                                                                                                                                                                                                                                                     PRALLGRKDCDFSFSGLKTAAARIAETLTTDD-----ARRDLAAGVQAAIARQLSE 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NLLNDTIVIAGGVAANKYLQEILSDCTRPYGYRLIAPPMHLCTDNAAMIAYAGLER 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KRTHRAILFCKO-----LLPQN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLGLGKYKILGTTIDDAVGETFDKVAKMLNL-----SFPGGPEIEKRAKLGNPHKYKF 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---NAVLVASGGVASNFYIRRALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIER 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKMQDAİRLYKQILNDYYEDINHPTKLNLKSFRKDEFNWKPLECITRPKYRIHIQNSYRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.2%; Score 237.5; DB 2
34.3%; Pred. No. 4.6e-14;
7ative 29; Mismatches 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.2%; Score 238; DB 2; Length 387; 29.7%; Pred. No. 4.4e-14; tive 32; Mismatches 74; Indels
                    Coulter,
                 A.L.; Mizoguchi, S.D.; Warrener, Coulter, S.N.; Folger, K.R.; Kas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                          Pseudomonas aeruginosa
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               Hickey,
Larbig,
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A; Residues: 1-341 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Gene: gcp; PA0580
;Superfamily: O-si
                                                                                                                                                                                                                                                                                                  Matches
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 308
                                    183
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 DNAAMIAYAGLER
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A;Gene: gcp
C;Superfamily: O-sialoglycoprotein endopeptidase
C;Keywords: hydrolase; metalloproteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RiOgata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: E97707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O-sialoglycoprotein endopeptidase (EC 3.4.24.57) [imported] - Rickettsia conorii C;Species: Rickettsia conorii C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001 C;Accession: E97707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Accession: H83572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-344 <KUR>
A;Cross-references: GB:AE006914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE004494; GB:AE004091; NID:g9946446; A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 406, 959-964, 2000
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                                                                                                                                                                                                                       198 PKPIINSGNCNMSFSGLKTAVRTLIMTLKEINDTV
                                                                                                                                                                                                                                                                                                                            145 VIGIGKYKIIGSTIDDAVGBAFDKVAKWINL-----APPGGPBIBKRAKIGDPHKYKF 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142 LVRVDGIGRYQLIGESVDDAAGEAFDKTAKLIGL-GYP-----GGPEIARLAERGTPGR 194
                                                      DNGIMIAWNGIER
                                                                                                          KRTHRAILFCKQ-RDLLPQNNAVLVASGGVASNFYIRRALBILTNATQCTLLCPPPRLCT 182
                                                                                                                                                                                                                                                                KPPLHHAKNCDFSFTGLQHVTDKIIMK-KEKEEGIBKGQILSSAADIAATVQHTMACHLV 123
                                                                                                                                                                                                                                                                                                                                                                       VQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TDNGIMIAWNGIERLRAGLGILHDIEGIRYEPKCPL 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLIKCRRAL---KQTGL--KN---LVIAGGVSANQALRSGLEKMLGEMKGQVFYARPRFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVKRTHRAILFCKORDLLPONNAVLVASGGVASNFYIRRALEILTNATOCTLLCPPPRLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TDNGAMIAYAGCQRLLAG---QHDGPAISVQPRWPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMACH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O-sialoglycoprotein endopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                            18.6%; Score 230.5; DB llarity 33.2%; Pred. No. 1.9e-1: Conservative 34; Mismatches
320
                                                   195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIDN:AAL02599.1; PID:g15619097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.9e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
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C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Accession: G69388
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: G69388
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-323 < KLE>
A; Cross-references: GB: I
C; Superfamily: O-sialogl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C;Accession: H64074
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, B.F.; Kerlavage, ; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D., Gocayne, J.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
Science 269, 496-512, 1995
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A; Residues: 1-342 <TIGR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMID:7542800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: nucleic acid sequence not shown; translation not shown
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Best Local S
Matches 67
                                                                                                                                                Query Match
Best Local 9
                                                                                                                                                                                                                          Superfamily: O-sialoglycoprotein endopeptidase
                                                                                                                                                                                                                                               Cross-references: GB:AE001027; GB:AE000782; NID:g2689350; PIDN:AAB90129.1; PID:g26494
                                                                                                                         Matches
                     142
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                  YRVFGETLDIGIGNALDKLARHMGL-KHP-----GGPKIEBLAKKGQKYHF--LP--YV 190
                                                                 FLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHH 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FCTDNGAMIAYTGFLRLKQG 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LCTDNGIMIAWNGIERLRAG 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRALEILTNATQCTLLCPPPR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEG--IEKGQILSSAADIAATVQHTMA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.1%; Score 224; DB 2; llarity 33.5%; Pred. No. 7.3e-13; Conservative 28; Mismatches 83
                                                                                                                      Conservative
                                                                                                                                              32.8%;
                                                                                                                      30;
                                                                                                                   Score 221.5; DB 2
Pred. No. 1.2e-12;
0; Mismatches 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GB:L42023; NID:g1573509; PIDN:AAC22187.1
                                                                                                                                                                   DB 2;
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th, T.; Connerton, P.; Croniu, A., ---
, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;

A;Title: Complete genome sequence of a multiple drug resistant

A;Title: Complete AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                      RESULT 12
G70369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable glycoprotease [imported] - Salmonella enterica subsp. enterica ser. C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AG0892
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AG0892
                                                               A;Title: The complete genome of the hyperthermophilic bacterium A;Reference number: A70300; MUID:98196666; PMID:9537320 A;Accession: G70369
                                                                                                                                                                                                          sialoglycoproteinase - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change
C;Accession: G70369
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A; Residues: 1-337 < PAR>
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                   A; Molecule
                                         A; Status: preliminary; nucleic
                                                                                                                                          Nature 392, 353-358, 1998
                                                                                                                                                                                    R; Deckert, G.; Warren,
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A;Residues: 1-335 <AQF>
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                   type: DNA
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Pred. No. 7.4e-12;
                                           sequence
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                                              shown;
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                                                                                                                                                                                         W.G.; Lenox,
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                                              translation
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Salmonella enterica
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                                                                                                                  Aquifex aeolicus
                                                                                                                                                                                         A.L.; Graham,
                                              not
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RESULT
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R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:O66986; GB:AE000708; NID:g2983356; PIDN:AAC06951.1; PID:g298
A;Experimental source: strain VF5
C;Genetics:
o-sialoglycoprotein endopeptidase C; Species: Pyrococcus abyssi
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C;Superfamily: O-sialoglycoprotein endopeptidase
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A; Residues: 1-337 < KUR>
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Best Local :
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                                                                                                                                                                                                                                                              122 LVKRTHRAILFCKORDLLPONN-AVLVASGGVASNFYIRRALEILTNATOCTLLCPPPRL 180
                                                                                                                                                                                                                                                                                                        195 FTFPRPMTDRPGLDFSFSGLKTFAANTIRANGDDD-----QTRADIARAFEDAVVDT 246
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                                                                                                                                                                                                                                                                                                                                                                                              142 LISVTGIGEYLLLGESVDDAAGEAFDKTAKLLGL-DYP-----GGPMLSRMAQQGTVGR 194
                                                                                                                                                                                                                                                                                                                                                 62 FDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMACH 121
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                                                                                                                                                                        CTDNGIMIAWNGIERLRAGLGILHDIEGIRYEPKCPL 217
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                                                                                                                                CTDNGAMIAYAGMVRLRSN---LNSELSVSVRPRWPL
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32.0%;
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J%; Pred. No. 1.2e-11;
41; Mismatches 73;
                    (gcp)
                      PAB1159 -
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                    Pyrococcus abyssi (strain
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R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Hgasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: C91122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004 (2;Accession: F75029 R;anonymous, Genoscope submitted to the EMBL Data Library, July 1999 A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chapters and the control of the EMBL Data Library, July 1999 R;Description: Pyrococcus abyssi genome sequence: insights into archaeal chapters are the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the 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A;Residues: 1-337 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB37370.1; PID:g13363420; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable O-sialoglycoprotein endopeptidase [imported] - Escherichia coli (strain O157:H7, C;Species: Escherichia coli (coli (strain O157:H7, C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 C;Accession: C91122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: gcp; PAB1159
C;Superfamily: O-sialoglycoprotein endopeptidase
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C;Superfamily: O-sialoglycoprotein endopeptidase
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A;Experimental source: strain Orsay
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A;Molecule type: DNA
A;Residues: 1-324 <KAW>
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A; Accession: F75029
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247
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                                                                                                                                                                             FVFPRPMTDRPGLDF6F6CLKTFANTT----RDNGTDD----QTKADIARAFEDAVVDT 246
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ative 34; Mismatches 90
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DLTGFKR---LVMAGGVSANRTLRAKLAEMMKKRRGEVFYARPEFC
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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## REFERENCE AUTHORS TITLE JOURNAL ACCESSION VERSION KEYWORDS SOURCE RESULT 1 BQ423651 LOCUS DEFINITION FEATURES COMMENT ORGANISM source Contact: NOWELL CONTROLL REMAIN: COMPAGE 1. NOW Email: cgapbs-remail.nih.gov Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC/DCTD/DTP CDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM13342 row: 1 column: 21 Plate: LLAM13342 row: 1 column: 21 BQ423651 870 b AGENCOURT 7790948 NIH MGC 72 H 5', mRNA sequence. BQ423651 GI:21118966 EST. I (bases 1 to 870) II (MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiens Homo sapiens (human) quality sequence stop: Location/Qualifiers /organism≂"Homo sapiens" /mol\_type="mRNA" /db\_xref="taxon:9606" clone="IMAGE:6065828" bp mRNA linear EST 23-PMAI-200. Homo sapiens cDNA clone IMAGE:6065828 Consortium (LLNL) linear information can EST 23-MAY-2002 þe

tissue\_type="melanotic melanoma"

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/clone lib="NIH MGC 72"
/note="Organ: skin; Tector: pCMV-SPORT6; Site 1: Not1;
Site 2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life Technologies."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: graeme@helix.nih.gov
Plate: 03 row: d column: 11
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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                       AlaLysAsnCysAspPheSerPheThrGlyLeuGlnHisValThrAspLysIleIleMet
                                                                              GAACATTTGGCCAAACAAGGAAATAGATTTCATTTTGACATCAAACCTCCCTTGCATCAT
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GCTAAAAATTGTGATTTTTCTTTTACTGGACTTCAACACGTTACTGATAAAATAATAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="Retina"
/dev_stage="Adult"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_lib="Human Retina cDNA (Un-normalized,
unamplified): hd/he"
/note="Organ: Eye; Vector: pSPORT1; Neural retina tissue
was dissected from two 80 year old donors with no observed
eye disease. 100ug of total RNA was used for library
construction. A directionally cloned cDNA library in the
pSPORT1 vector (Life Technologies) was constructed at
Bioserve Biotechnology (Laurel MD) essentially following
the protocols of the SuperScript Plasmid System full
details of which are contained in the manufacturer's
Instruction manual (http://www.lifetech.com/). First
strand synthesis was carried out using a Not I
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="hd03d11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [5'-pGACTAGTTCTAGATCGCGAGCGGCCGCC(T)15-3']. EST analysis
was performed on the unamplified library at the NIH
Intramural Sequencing Center (NISC).
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                               Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y., RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipcline with 364 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                        Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected soluble to prepare full-length cDNA libraries for rapid discovery of new captains.
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Meth. Enzymol. 3
99279253
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                               polyA_site
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Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kori, F., Kurihara, C., Matsuyama, T., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Myazaki, A., Murata, M., Koya, S., Kurihara, C., Matsuyama, T., Myazaki, A., Murata, M., Nishi, K., Nomura, K., Numazaki, R., Ohoo, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tanaka, T., Tomaru, A., Takahashi, F., Takaku-Akahira, S., Muramatsu, M., and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (16-UUL-2001) Yoshihide Hayashizaki, The Institute of Submitted (16-UUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (Gs. RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokokanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9216)
Pax:81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prepare mouse tissues.
Please visit our web site for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in R.
Genomic Sciences Center and Genome Science Laboratory in RIKEN
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Analysis of the mouse transcriptome based on of 60,770 full-length CDNAs
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Functional annotation of a full-length mouse
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URL:http://fantom.gsc.riken.jp/.
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                                                                  /protein_id="BAC32450.1"
/db_xref="G1:26337529"
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scddygaavvdbetgnvl.gralibschyvhlktyggivppvaQQlhreniqrivbetlsac
Ritpsdlsalatikpcyglspslolvnopfkcpfiplhmarhatirltnk
vbppplublisgghcllalvQguspplligksldlapgdhldkvarrlslikhbesti
wsggkalbolakognrehftinppmQnakncdpsptglditdblitdblithkbksbloibkg
gilssbadiaavQhatachlakrthbailfckQknllspanavlysggvasnlyir
QilssbadiaaavQhatachlakrthbailfckQknllspanavlysggvasnlyir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="unnamed protein product; putative similar to PUTATIVE SIALOGLYCOPROTEASE TYPE 2 sapiens] (SPTR|Q9H4B0, evidence: FASTY, 80%ID,
GVDISREVABAAIKVPRLKMAL"
                                     KALEIVANATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGVLHDVEDIRYEPKCPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="C57BL/6J"
/db_xref="FANTOM_DB:B230219017"
/db_xref="taxon:10090"
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                                                                           Mus
Mus
                                                                                                                                                                                                 AK011265 mRNA linear HTC 03-APR-Mus musculus 10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2610001M19 product:similar to PUTATIVE SIALOGLYCOPROTEASE TYPE 2 [Homo sapiens], full insert sequence.
                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                    AK011265.1 GI:12847275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itch, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, X., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Yoshino, M., Muramatsu, M., and Hayashizaki, The Institute of Submitted (10-JUL-2000) Yoshihida, K., The Submitted (10-JUL-2000) Yoshihida, K., T., Washizaki, The Institute of Landau, A., Shinagawa, A., Shinagaki, The Submitted (10-JUL-2000) Yoshihida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, Y., Yoshida, Y., Yoshida, Y., Yoshida, Y., Yoshida, Y., Yoshida, 
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                                                                   Physical and Chemical Research (RIKEN), Laboratory for Gen
Exploration Research Group, RIKEN Genomic Sciences Center
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Pax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Group Phase I & II Team.
Analysis of the mouse transcriptome based of 60,770 full-length cDNAs
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6 (bases 1 to 1622)
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                                                 with XhoI and SstI. Cloning sites, 5'
                                                                                                                                                                                                                                                                                                    cDNA library was prepared and sequenced in Mouse Genome
                                                                                                                                                                                                                                                                                                                                                           Please visit our
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                          GlnAsnAsnAlaValLeuValAlaSerGlyGlyValAlaSerAsnPheTyrIleArgArg 160
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/db xref="G1:12847276"
/db xref="G1:12847276"
/translation="MLMLRRTAGAIPKPRESKYYGFLRRFSVHPRTLSCHKLVLGIET
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VEFPFLVLLISGGHCLLALVQGVSDFLLLGKSLDIAFGDMLDKVARRLSLIKHPECST
MSGGKALEQLAKUGNRFHFTINPPMQNAKNCDFSFTGLQHITDKLITHKEKEGIEKE
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GILSSAADIAAAVQHATACHLAKRTHAAILFCKQKNLLSPANAVLVVSGGVASNLYIR
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similar to PUTATIVE SIALOGLYCOPROTEASE TYPE 2 [Homo
sapiens] (SPTR|Q9H4B0, evidence: FASTY, 80%ID, 100%length,
match=1242)"
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/db_xref="FANTOM_DB:2610001M19"
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clone_Tib="RIKEN full-length enriched mouse cDNA library"
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1 LeuLeuAlaLeuValGlnGlyValSerAspPheLeuLeuGlyLysSerLeuAspIle 20

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Query Match:
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BX39199 Homo sapiens HELA CELLS
CDNA clone CSODKOO1YEO2 3-PRIME,
BX391919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 852)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On May 13, 2003 this sequence version replaced gi:30611736.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOBAIO35ZEO7_CSO3317_1&c=1240.r
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlyIleLeuHisAspIleGluGlyIleArgTyrGluProLysCysProLeuGlyValAsp 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCATTGGAAATTGTCGCAAATGCAACGCAGTGCACGTTGTTGTGTCCACCTCCAAGACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATATCCAGAGAAGTTGCAGAAGCTGCCATAAAAGTACCGCGATTAAAAATGGCACTT 1448
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                                                                                                                                                                                                                                           /clone lib="Homo sapiens HELA CELLS COT 25-NORMALIZED" /note="1st strand cDNA was primed with a NotI-oilgo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol type="mRNA"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone="CSODKO01YEO2"
/cell type="HELA CELLS COT 25-NORMALIZED"
/cell_line="HELA"
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                                                                 2.28e-97
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ELA CELLS COT 25-NORMALIZED Homo sapiens
3-PRIME, mRNA sequence.
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                                                                                                            Length:
Matches:
Conservative:
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                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. CE 1 (bases 1 to 1609)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Buffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Schers, R.M., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
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Mus musculus O-sialoglycoprotein
clone IMAGE:1226118), containing
2 (bases 1 t
Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                       Proc. Natl. Acad. Sci. U.S.A.
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                                                                                                              human and mouse cDNA sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     musculus (house mouse)
                                                                                     99 (26), 16899-16903 (2002)
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21312463
This clone has the following problem: frame shifted.

Location/Qualifiers
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Tissue Procurement: Marcello Bento Soares, Ph.D.
cDNA Library Preparation: M. Bento Soares, University of
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNI)
DNA Sequencing by: Institute for Systems Biology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton,
Madan, Stephanie Rodrigues, Amy Sanchez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: MGC help desk
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                             HisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuPro 140
                                                                                                                GlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThrValGlnHisThrMetAlaCys
                                                                                                                                                                                                     LeuGlnHisValThrAspLysIleIleMetLysLysGluLysGluGluGlyIleGluLys 100
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                                                                                           GGGCAAATCCTGTCATCAGCTGCAGACATTGCTGCTGCGGTACAGCATGCAACAGCGTGC
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/clone="IMAGE:1226118"
/tissue type="Thymus gland, mouse"
/clone_Tib="Soares_thymus_2NbMT"
/lab host="DH10B"
/note="Vector: pT7T3-Pac"
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/mol_type="mRNA"
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High quality sequence stop: 701.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph. Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP
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601595739F1 NIH_MGC_9
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Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.
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                                                                                                                                                            /clone="IMAGE:3949640"
/tissue_type="adenocarcinoma cell line"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 9"
/clone_lib="NIH MGC 9"
/note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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908.00
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   source
               Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called wi
trimmed with the aid of the trim_alt op
cross_match v0.990329.
Plate: SRG8015 row: H column: 12
Seq primer: TAGAAGGCACAGTCGAGG.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                   CF362328 658 bp mRNA 829596 MARC 3PIG Sus scrofa cDNA 3', mRNA CF362328 CF362328.1 GI:34161882 EST. Sus scrofa (pig)
                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 658)
Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Fox, J., Wise, T.A., Nonneman, D.J., Wray, J.E. and Keele, J.W. A. second set of porcine ESTs from a pooled-tissue normalize;
                                                                                                                                                                                                                   Unpublished (2003)
Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _
                                                                                                                                               USDA, ARS, US Meat Animal PO Box 166, Clay Center, N Tel: 402 762 4366 Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                         Sus scrofa
                                                                                                                                                                                                                                                           library
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on. Vector identi
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with

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Query Match:
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DEFINITION
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                            ORGANISM
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Bos taurus (cow)
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                            sequence.
CK941819
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4065407 BARC 10BOV
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                                                                                                                                                                                                                                                                                              AlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysProProProArgLeu 180
                                                                                                                                                                                                                                                                                                                                                                                                                                HisLeuValLysArgThrHisArgAlaIleLeuPheCysLysGlnArgAspLeuLeuPro 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CysSerThrMetSerGlyGlyLysAlaIleGluHisLeuAlaLysGlnGlyAsnArgPhe 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 3PIG"
/note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
/note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
/ibrary_made_with_RNA pooled_from_multiple_tissues
including_brain, liver, muscle, placenta/endometrium,
ovary, testes, and bone_marrow."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.07e-91
876.00
93.68%
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                                                                                                                              Bos taurus
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aurus cDNA
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Matches:
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                                                                                                                                                                                                                                                                     94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Tad S. Sonstegard
Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute
Bdlg. 200 Rm2A BARC-East, Beltsville, MD
Tel: 3015048416
Fax: 3015048414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Single pass sequencing. Bases called and trimmed with phred 0.000925 using options -trim_alt " -trim_fasta. Vector ident by cross match using options -minmatch 12 -minscore 18 Plate: 12 row: F column: 24
Seq primer: AGCGGATAACAATTTCACACAGG
High quality sequence stop: 637.
Location/Qualifiers
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Sonstegard, T.S., Van Tassell, C.P., Matukumalli, L.K., Harhay, G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.
Production of EST from cDNA libraries derived from immunologically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: tads@anri.barc.usda.gov
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SerABnPheTyrI1eArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCy8ThrLeu
                                                                                     LysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyValAla 153
                                                                                                                                                               ValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArgAlaIleLeuPheCys 133
                                                                                                                                                                                                                                                    LysGluGluGlyIleGluLysGlyGlnIleLeuSerSerAlaAlaAspIleAlaAlaThr 113
                                                                                                                                                GTGCAGCACCGTGGCCTGCCACATTGCAAAAAGAACACATCGTGCTCTTCTGTTCTGC
                                                                                                                                                                                                                                 AAAGAGGAAGGTATCGAGCAGGGGCAGGTCCTGTCTTCAGCTGCAGACATTGCTGTTGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="Multiple"
/lab_host="DH10B Tl phage resistant"
/clone_lib="BARC 10BOV"
/clone_Stage="BARC 10BOV"
/note="Torgan: Small Intestine; Vector: pagen-1; Site_1:
ECORV; Site_2: NotI; Equimolar amounts of mRNA extracted
from proximal jejunums of 18 and 21 wk old steers, and
distal ileums of 14 day old calves. proximal jejunum
exposed to C. oncophora for 3 and 6 weeks, and distal
ileum exposed to C. parvum for 7 days"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue_type="Pooled"
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/clone="10BOV12_F24"
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/strain="Holstein"
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1 (bases 1 to 922)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
                                                                                                                                                                                                                                                                                                                                                                                 found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov plate: LLCM2603 row: d column: 15 High quality sequence stop: 584. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            922 bp AGENCOURT 8863711 NIH MGC 18 Homo 5', mRNA sequence
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BQ961028.1 GI:22376506
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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                                                                                                                                                   /clone="IMAGE:6423902"
/tissue_type="large_cell_carcinoma"
/tissue_type="large_cell_carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 18"
/clone_lib="NIH MGC 18"
/clone_lib="NIH MGC 18"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
/coRI; CDNA made by oligo-df priming. DTrectionally cloned
into EccRI/XhoI sites using the following 5' adaptor:
into EccRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
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               Shirakawa Institute of Animal Genetics Odakura, Nishigo, Nishi-shirakawa, Fukn Tel: 81-248-25-5641
                                                        Contact: Yoshikazu Sugimoto
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Nucleic Acids Res. 29
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Takasuga, A., Hirotsune, S., Itoh, R., Jitohzono, A., Suzu
and Sugimoto, Y.
Bstablishment of a high throughput EST sequencing syst
poly(A) tail-removed cDNA libraries and determination
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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CB852881 490 bp mRNA linear EST 22-AI UI-CF-FNO-afo-b-03-0-UI.81 UI-CF-FNO Homo sapiens cDNA clone UI-CF-ENO-afo-b-03-0-UI 3', mRNA sequence.
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Single pass sequencing.
This clone was obtained from a p
                                                                                                        4
                                                                                                                                                                 uArgAlaGlyLeuGlyIleLeuHisAspIleGluGlyIleArgTyrGluProLysCysPr 216
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                                                                                                                                                                                                                                                                                                                                                                  eTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThrLeuLeuCysPr 176
                                                                                                                                                                                                                                                                                                                                                                                                                              gAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyValAlaSerAsnPh 156
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/note="Vector: pZL1; Site_1: Sal1; Site_2: Not1; Poly
was deleted from a Not1 site"
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/dev_stage="fetus"
/lab_host="DH10B"
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/db_xref="taxon:9913"
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Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approximations of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the cont
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Tel: 319 356 4866
Fax: 319 356 7171
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McCray Lab
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Mammalia; Butheria; Primates; Catarrhini; Hominidae;
AlaIleLeuPheCysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAla
                                                                                                        AspIleAlaAlaThrValGlnHisThrMetAlaCysHisLeuValLysArgThrHisArg
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/tissue_type="Human Lung Epithelial cells"
/lab host="DH10B (Life Technologies) (T1 pl
/clone_lib="UI-CF-FNO"
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/db_xref="taxon:9606"
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1 (bases 1 to 822)
Wittzell, H., Bed'Hom, B., Morin, V., Yo Chausse, A.M. and Zoorob, R.
A collection of chicken ESTs from act Unpublished (2003)
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Gallus gallus
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Location/Qualifiers
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/db xref="taxon:9031"
/cell_type="Splenocytes"
/clone lib="PHA-activated s
/note="Vector: pTriplEX2"
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I BU127463.1 GI:25338728

I BU127463.1 GI:25338728

ST. Gallus (chicken)

Gallus gallus

Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

I (bases 1 to 866)

Boardman, P.B., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,

Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

TTLE

A Comprehensive Collection of Chicken cDNAs

Ourr. Biol. 12 (22), 1965-1969 (2002)
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                                                                                                                                                   Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute
                                                                                                               PO Box 88, Manchester, Tel: 01612008930
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                                                                         Simon.Hubbard@umist.ac.uk
Location/Qualifiers
           /organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, H
/db_xref="taxon:9031"
                                                                1. .866
 clone="ChEST66m2"
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                     IleSerLysGluValGlyGluAlaSerIleLysValProGlnLeuLys 236
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//cione lib="CSEQCHL20"
//note="Organ: limbs; Vector: pBluescript II KS(+); Site 1:
BCORI, Site 2: Not1; Modification of pBluescript II KS(+)
[Stratagene] vector to accommodate cDNA produced with the
T-trimmed protocol (Construction of uni-directionally
cloned cDNA libraries from messenger RNA for improved 3'
end DNA sequencing by Glenn Ru, et al. U.S. Patent #
6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.
Ligate in double stranded adaptor containing BsgI and
BamHI sites [5'ggccgcgtgcacgcg]"
[5'aattctttttttcggatccgggctgcacgc]"
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80
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                                            61
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                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Howard Jacobs
CDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM.1944 row: d column: 02
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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Bldg. 31 Rm10A07 Bethesda, MD 20892
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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736 bp mRNA linear EST 23-AGENCOURT 17157291 NIH MGC 231 Rattus norvegicus cDNA clone MAGE:7097620 5', mRNA sequence.
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//clone lib="NIH MGC 231"
//clone lib="NIH MGC 231"
//note="Organ: lung; Vector: pExpress-1; Site_1: EcoRV;
//note="Organ: lung; Vector: pExpress-1; Site_1: EcoRV;
Site_2: Not1; RNA obtained from pooled lung tissue from a mix of male and female animals at 8 wk old. Tissues were snap-frozen and kept at -80°C for two days before RNA extraction and purification (Tri-reagent method). cDNA was primed using oligo-dT primer:
5'-pGACTAGTICTAGAICGCCAGCGGCCGCCC(T) 25-3' and cloned into the EcoRV/NotI sites of pExpress-1. Size-selection >1.4kb resulted in an average insert size of 2.3 kb. This primary library is not normalized (normalized primary library is library is constructed by Express Genomics (Frederick, MD). Note: this is a NIH_MGC library."
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/lab_host="DH10B TonA"
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/db_xref="taxon:10116"
/clone="IMAGE:7097620"
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CCACGATTAAAAATGACACTT 501
CCAAAATGTCCTCTCGGAATAGACATATCCAGAGAAG ProGlnLeuLysMetGluIle 239
ProLysCysProLeuG1yValAspIleSerLysGluValG1yGluAlaSerI1eLysVal
ATTGAAAGATTACGTGCTGGCTTGGGCATTTTACATGATGTAGAAGACATCCGATACGAA
IleGluArgLeuArgAlaGlyLeuGlyIleLeuHisAspIleGluGlyIleArgTyrGlu
TTGTTGTGTCCCCCTCCGAGACTGTGCACTGACAATGGTATCATGATTGCATGGAATGGA
LeuLeuCysProProArgLeuCysThrAspAsnGlyIleMetIleAlaTrpAsnGly 192
GCAAGTAACTTGTACATCCGAAGAGCATTGGAAATTGTAGCAAATGCAACACAATGCACT
AlaSerAsnPheTyrIleArgArgAlaLeuGluIleLeuThrAsnAlaThrGlnCysThr 172
TGCCAGCAGAAAATTTGCTATCTCCAGCTAACGCAGTATTAGTTGTGTGTCTGGAGGTGTT 240
CysLysGlnArgAspLeuLeuProGlnAsnAsnAlaValLeuValAlaSerGlyGlyVal

Search completed: February 16, 2005, 21:04:55 Job time : 2847.68 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

February 16, 2005, 10:46:17; Search time 40.5261 Seconds
(without alignments)
3019.954 Million cell updates/sec

Title:
Perfect score: 1240
Sequence:

1 LLALVQGVSDFLLLGKSLDI.......DISKEVGEASIKVPQLKWEI 239

Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5

Searched:
1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters:
1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:
UniProt_03:*
1: uniprot_tsprot:*
2: uniprot_tsprot:*
2: uniprot_trembl:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Q9abz9 caulobacter	Q9zea8 rickettsia				Q8yjb1 brucella me			Q68xr3 rickettsia	Q6nd54 rhodopseudo		Q7w668 bordetella	acinetobac		Q73h71 wolbachia p	Q7vxn4 bordetella	Q921h8 rhizobium m		-		drosophila		Q8jfr7 brachydanio			ratt	0 mus	Butt	mus m		Q96ev9 homo sapien	ription	

45	44	43	42	41	40	39	38	37	36	35	34	<b>ω</b>	32
217	219.5	221.5	223.5	224	224	228.5	230.5	231	231	231	233.5	234.5	236.5
17.5	17.7	17.9	18.0	18.1	18.1	18.4	18.6	18.6	18.6	18.6	18.8	18.9	19.1
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Q8esi6	Q8xx97	029153	Q65rp0	P43764	Q82xn2		Q92jk6			Q7nue3	Q61v10	Q7pag7	. Q89ww1
oceanobacil	ralstonia s				nitrosomona		rickettsia			chromobacte	photobacter	rickettsia	bradyrhizob

## ALIGNMENTS

	RC TISSUE=Muscle; RX MEDLINE=2238857; RA Strausberg R.L., RA Strausberg R.L., RA Altschul S.F., Ze RA Altschul S.F., Ze RA Hopkins R.F., Jor RA Diatchenko L., Ma RA Stapleton M., Soa RA Stapleton M., Soa RA Brownstein M.J., RA Raha S.S., Loquel RA Richards S., Worle RA Richards S., Worle RA Richards S., Worle RA Whiting M., Madan RA Whiting M., Madan RA Blakesley R.W., T RA Rodriguez A.C., G RA Krzywinski M.I., RA Jones S.J., Marra RT and mouse cDNA se RL Proc. Natl. Acad.	SUL SUL
FROM N.A.  g.cle; g.cle; g.cle; g.cle; g.cle; (JUL-2001) to the EMBL/GenB. 11904; AAH11904.1; 12.004; 12.004; 12.004; 12.004; 12.004; 12.004; 12.004; 12.004; 12.004; 12.0078; Peptidase M22; 1. 12.0078; OSIALOPTASE. 100739; OSIALOPTASE. 100739; GENELOPTASE. 1007367; Peptidase_M22; 1. 171GR00329; gcp; 1. 171GR00329; gcp; 1.	scle;  gR.L., Feingold E.A., Groung R.D., Collins F.S., Wagner J. S.F., Zeeberg B., Buetow K.J. F., Jordan H., Moore T., M. D. L., Marusina K., Farmer A. M., Soares M.B., Bonaldo M. M.J., Usdin T.B., Toshiyul, Loquellano N.A., Peters G., McEwan P.J., McKernan K., G., McEwan P.J., McKernan K., G., McEwan P.J., McKernan M., McBwan P.J., McKernan M., Goergren Helton E., Ketteman M., Green Helton S., Ketteman M., Green Helton S., Ketteman M., Green Helton S., Ketteman M., Green Helton S., Ketteman M., Green Helton S., Ketteman M., Green Helton S., Ketteman M., Green Helton S., Ketteman M., Green Helton S., Ketteman M., Green Helton S., Ketteman M., Green M., Touchan J.W., Green A.C., Grimwood J., Schmutz i M.I., Skalska U., Smailus i M.I., Skalska U., Smailus on and initial analysis of CDNA sequences.",	PRELIMINARY; PRT; 414 A (TrEMBLrel. 19, Created) (TrEMBLrel. 19, Last sequence (TrEMBLrel. 26, Last annotatio ein. (Human). (Human). tetazoa; Chordata; Craniata; Ve theria; Primates; Catarrhini; 606;
ank/DDBJ databases. endopeptidase activity; IEA. EA. Lidolysis; IEA.	See L.H., Derge J.G., L. Shenmen C.M., Schuler G.D., L., Shenmen C.M., Schuler G.D., H., Schaefer C.F., Bhat N.K., lax S.I., Wang J., Hsieh P., L.A., Rubin G.M., Hong L., L.F., Casavant T.L., Scheetz T.E., ki S., Carninci P., Prange C., L.J., Abramson R.D., Mullahy S.J., J., Malek J.A., Gunaratne P.H., J., Malek J.A., Gunaratne P.H., larcia A.M., Gay L.J., Hulyk S.W., E.J., Lu X., Gibbs R.A., E.J., Lu X., Gibbs R.A., E.J., Lu X., Gibbs R.A., E.J., Du X., Gibbs R.A., E.J., Du X., Gibbs R.A., E.J., Dickson M.C., E.D., Dickson M.C., D.C., Myers R.M., Butterfield Y.S., J. Myers R.M., Butterfield Y.S., D.E., Schnerch A., Schein J.E., more than 15,000 full-length human	AAA. De update) Dion update) Vertebrata; Euteleostomi;

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Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ295148; CAC14666.1; -.

REMEL; AJ295148; CAC14666.1; -.

REMECPS; M22.004; -.

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                                                                                                              ---EKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASN 155
                                                                                                                                                                                                                      HFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIFLISKVEQINIPGLCLKIAAHF 295
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                                                                        CRYEKGQILSSAADIAATVQHTMACHLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASN
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FYIRRALEILTNATQCTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDIEGIRYEPKC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>.</u>
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Pred. No. 1.3e-98;
0; Mismatches 1; Indels 25;
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RP SEQUENCE FROM N.A.

RC STRAIN=CZECH II; TISSUB=Mammary tumor;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

RA Hopkins R.F., Jordan H., Max S.I., Wang J., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gy L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gy L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gy L.J., Hulyk S.W.,

RA Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Hitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Mortinguez A.C., Grimwood J.W., Green E.D., Dickson M.C.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Krzywinski M.S., Salska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                Query Match
Best Local S
Matches 205
                                                                                                                                                                                                                                                                   L Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.

R EMBL; BC058172; AAH58172.1; -

R GO; GO:0008450; F:O-sialoglycoprotein endopeptidase activity; IEA

R GO; GO:0008270; F:zinc ion binding; IEA.

R GO; GO:0008270; F:zinc ion binding; IEA.

R GO; GO:0008270; F:proteolysis and peptidolysis; IEA.

R GO; GO:0008508; P:proteolysis and peptidolysis; IEA.

R InterPro; IPR000905; Peptidase M22.

InterPro; IPR009180; Peptidase M22.

R InterPro; IPR009180; Peptidase M22; 1.

R PIASF; PIASF004537; Osialglc.pptds; 1.

R PIASF; PIASF004537; Osialglc.pptds; 1.

R PIASF; PIASF004537; Peptidase M22; 1.

R PIASF; PIASF004537; Peptidase M22; 1.
                                                                                                                                                                                                                                Hypothetical protein. SEQUENCE 414 AA; 4
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=CZECH II; TISSUE=Mammary tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein. Mus musculus (Mouse).
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                       61
                                                              Similarity
HFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMAC
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                                                                                                                                                                                                                                  44962 MW;
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Last annotation updat
                                                                                                                                                                    Score 1086; DB 2;
Pred. No. 2.2e-87;
                                                                                                                                                                                                                                  0418AD93C6FEBCAE CRC64;
                                                                                                                                                     Mismatches
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SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;

STRAINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

Carninci P., Hayashizaki Y.;

"High-efficiency full-length cDNA cloning.";

Meth. Enzymol. 303:19-44(1999).
                                                                                                                STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
MEDLINE-20530913, PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE-20530913, PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
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Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa Y., Izawa T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
"RIKEN integrated sequence analysis (RISA) system-384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length
enriched library, clone:B230219017 product:similar to PUTATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carminci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., In Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the RIKEN Genome Exploration Research Group Phase I & II "Analysis of the mouse transcriptome based on functional 60,770 full-length CDNAs.";
Nature 420:563-573(2002).
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01-MAR-2003
   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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STRAIN=C57BL/6J; TISSUE=Corpora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKEN FANTOM Consortium;
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                                                                 pipeline with 384 multicapillary
. 10:1757-1771(2000).
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Best Local
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Name=Osgepl1;

Mus musculus (Mouse).

Metazoa; Chordata;

"haria; Rodentia;
                                                                                                                                                                                                                                                                                                                 01-MAR-2004 (TERMBLrel. 26, Last sequence update)
Mus musculus 10 days embryo whole body cDNA, RIKEN enriched library, clone:2610001M19 product:similar tSIALOGLYCOPROTEASE TYPE 2.

Name=Osgepl1:
SEQUENCE FROM N.A.

STRAIN-C57BL/63; TISSUE-Whole body;

MEDLINE-99279253; PubMed=10349636; DOI=10.10

Carninci P., Hayashizaki Y.;

"High-efficiency full-length cDNA cloning.";

Meth. Enzymol. 303:19-44(1999).
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01-JUN-2001 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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GO; GO:0008270; F:zinc ion binding; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR000905; Peptidase M22.
InterPro; IPR00905; Peptidase M22.
InterPro; IPR00905; Peptidase M22.
InterPro; IPR00905; Peptidase M22.
InterPro; IPR00905; Peptidase M22.
InterPro; IPR00905; Peptidase M22.
InterPro; IPR0090537; Osialgl. Dptds; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9D0N0;
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9D0N0
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ProDom; PD002367; Peptidase M22; 1.
TIGRPAMs; TIGR00329; gcp; 1.
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                                                                                                                                                                                                NCBI_TaxID=10090;
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Pred. No. 9.1e-87;
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Sciurognathi;
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                                                                                        DOI=10.1016/S0076-6879(99)03004-9;
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                                                                                                                                                                                                                                    Vertebrata;
:hi; Muridae;
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to PUTATIVE
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; Murinae; Mus
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C STRAIN=C57BL/6J; TISSUE=whole body;

MEDLINE=20530913; PubMed=11076861; DDI=10.1101/gr.152600;

A Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carminci P.,

A Konno H., Akyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

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L Genome Res. 10:1757-1771(2000).
                                                                                                                               MEROPS; M22.004; -...

R MGD; MGI:1919335; Osgep11.

R GO; GO:0008450; F:O-sialoglycoprotein endopeptidase activity; IEA.

R GO; GO:0008233; F:peptidase activity; IEA.

R GO; GO:0008270; F:zinc ion binding; IEA.

R GO; GO:0008270; F:zinc ion binding; IEA.

R GO; GO:0008270; F:peptidase M22.

R InterPro; IPR000905; Peptidase M22.

R InterPro; IPR000905; Peptidase M22; 1.

R Pfam; PF00814; Peptidase M22; 1.

R Pfam; PF00814; Peptidase M22; 1.

R PRINTS; PINSF004537; Osialglc_pptds; 1.

R PRINTS; PR00789; OSIALOPTASE.

R PRINTS; PR00789; OSIALOPTASE.

R PTIRPAMS; TIGR00329; gcp; 1.
                         Query Match
Best Local S
    Matches 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-C57BL/6J; TISSUE-Whole body;
Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carrinci P., Pukuda S., Pukunishi Y., Furuno M.,
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Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
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Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.,
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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STRAIN=C57BL/6J; TISSUB=Whole body;

STRAIN=C57BL/6J; TISSUB=Whole body;

MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

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Genome Res. 10:1617-1630(2000).
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STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AK011265; BAB27506.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Functional annotation of a full-length mouse cDNA collection.";
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                       Local Similarity
                                                                                          414 AA;
Conservative
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                                                                                          44999 MW;
                       86.4%;
; Score 1071; D; Pred. No. 4.6e
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                    1; DB 2;
4.6e-86;
                                         Length
  Indels
                                              414;
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           L Submitted (AUC-2004) to the EMBL/GenBank/DDBJ databases.

R EMBL; BC078974; AAH78974.1; -.

R GO; GO:0008450; F:O-sialoglycoprotein endopeptidase activity; IEA

R GO; GO:0008270; F:zinc ion binding; IEA.

R GO; GO:0008508; P:proteolysis and peptidolysis; IEA.

R GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

R InterPro; IPR00905; Peptidase M22.

R InterPro; IPR009180; Peptidase M22.

R InterPro; IPR009180; Peptidase M22.

R InterPro; IPR002016; Peroxidase.

R Ffam; PF00814; Peptidase M22; 1.

PF1RSF; PIRSF004537; Osialglc_pptds; 1.

RRINTS; PR007189; OSIALOPTASE

DR PROSITE; PS00435; PEROXIDASE_1; UNKNOWN_1.
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RC TISUE-Testis;

RX PubMed=12477932; DOI=10.1073/pnas.242603899;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RIA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

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RA Altschul S.F., Zeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

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RA Holling M.T., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Generation and initial analysis of more than 15,000 "Generation and initial analysis of more than 15,000 and mouse cDNA sequences.";

NATE YMPACHAGE TO MAIL Acad. Sci. U.S.A. 99:16899-16903(2002).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-MAR-2004 (TrEMBLrel. 26, Last annotation updat
Hypothetical protein FLJ30879.
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Best Local Sim
Matches 186;
Query Match
Best Local Similarity
Matches 146; Conserv
                                                                                                                                                  GO; GO:0008450; F:O-sialOglycoprotein endopeptidase act
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0008270; F:zinc ion binding; IEA.
GO; GO:0006570; F:zinc ion binding; IEA.
InterPro; IPR00905; Peptidase M22.
InterPro; IPR009180; Peptidase M22.
InterPro; IPR009180; Pept M22 Osialgl.
Pfam; PF00814; Peptidase M22; 1.
PFIRSP; PIRSP004537; Osialglc_Dptds; 1.
PRINTS; PR00788; OSIALOPTASE.
PRODOm; PD002367; Peptidase M22; 1.
TIGGPAMs; TIGR00329; gcp; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Babbage A.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases
EMBL; AL591593; CAD43471.1; -.
MEROPS; MZZ_004; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=7955;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8JFW3;
01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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GO; GO:000823; F:peptidase activity; IEA.
GO; GO:0008270; P:Zinc ion binding; IEA.
GO; GO:0008508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR009105; Peptidase M22.
InterPro; IPR009180; Peptidase M22.
InterPro; IPR009180; Peptidase M22.
PFam; PF00814; Peptidase M22; 1.
PIRSF; PIRSF004537; Osialglc pptds; 1.
PRINTS; PR00789; OSIALOPTASE.
PRODOM; PD002367; Peptidase M22; 1.
TIGRPAMS; TIGR00329; gcp; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                             404
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                      60.6%;
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98.4%;
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Last annotation updat
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Score 751; DB 2; Length 404; Pred. No. 7.9e-58; indels 2; Mismatches 59; Indels
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Pred. No. 2.5e-76;
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                                                                                                           3A6B1DD050737E35 CRC64;
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Matches 145
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GO; GO:0008270; F:peptidase activity; IEA.
GO; GO:0008270; F:zinc ion binding; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001905; Peptidase M22.
InterPro; IPR001905; Peptidase M22.
InterPro; IPR0019180; Pept M22 GSialgl.
Pfam; PF00814; Peptidase M22; 1.
PIRSF; PIRSF004537; OsiaIoPFTASE.
PRINTS; PRO0709; OSIALOFTASE.
PROO709; DO02267; Peptidase M22; 1.
TIGRPAMs; TIGR00329; gcp; 1.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
SI:dZ72B14.6 (Novel glycoprotease).
Name=SI:dZ72B14.6;
Brachydanio rerio (Zebrafish) (Danio rerio).
Buxachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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Q8JFR7;
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                                                                          HLVKRTHRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRALBILTNATQCTLLCPPPRL 180
                                                                                                                                             HFDIKPPLHHAKNCDFSFTGLQHVTDKIIMKKEKEEGIEKGQILSSAADIAATVQHTMAC 120
                                                                                                                                                                                                     LLALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRF 60
              CTDNGIMIAWNGIERLRAGLGILHDIEGIRYEFKCFLGVDISKEVGEASIKVFQLKM 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTDNGIMIAMNGIERLRAGIGILHDIEGIRYEPKCPLGVDISKEVGEASIKVPQLKM 237
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                                                           HLAKRTHRAILFCKSKGLLPEQNPTLIVSGGVASNEYIRQILKIITDATGLHLLCPPSKF
                                                                                                                        AFHFISPMGQNYDCNFSFAGLRTQITGAINKKEKEEGVEAGQFLSCVKDIAAASQHTVAS
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Conservative
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Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
-!- EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry w)
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Name=agCG46164; ORFNames=ENSANGG00000007922;

Anopheles gambiae str. PEST.

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.

NCBI_TaxID=180454;
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36.3%; Pred. No. 1.9e-23;
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A Adams M.D., Celniker S.B., Holt R.A., Evans C.A., Gocayne J.D.,
A Amanatides P.G., Scherer S.B., Li P.W., Hoskins R.A., Galle R.F.,
A George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,
A Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
A Wan K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Gabor G.L.,
A Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
A Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
A Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Eugan D.A., Butler H., Cadieu E., Center A., Chandra I.,
A Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P.,
A Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
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GO; GO:0008450; F:O-sialoglycoprotein endopeptidase activity;
GO; GO:0008270; F:zinc ion binding; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR000905; Peptidase M22.
InterPro; IPR000905; Peptidase M22.
Flam; PP00814; Peptidase M22; 1.
Pfam; PF00814; Peptidase M22; 1.
PIRSF; PIRSF004537; Osialglc pptds; 1.
PRINTS; PR00789; OSIALOPTASE.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Droch; Brachycera; Muscomorpha;
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Last sequence update)
Last annotation updat
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RA Durbin K.J., Evangelista C.C., Ferriera S., Fleischmann W., RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C., RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C., RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Kimmel B.B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., RA Liu K., Mattei B.M., Keltosh T.C., McLeod M.P., McPherson D., RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., RA Melson D.R., Nelson K., Nusekern D.R., Pacleb J.M., RA Palazzolo M., Pitman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H., RA Spier B., Spradling A.C., Stapleton M., Skupski M.P., Smith T., RA Spier B., Spradling A.C., Stapleton M., Skupski M.P., Smith T., RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Wang S., Jao Q.A., Ye J., RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., The genome sequence of Drosophila melanogaster.";

RT "The genome sequence of Drosophila melanogaster.";

RT "The genome sequence of Drosophila melanogaster.";
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                                                                                                                                                                                                                                                                                                                                                                                            MEDIINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                      Submitted (MAR-2004) to the EMBL; AE003513; AAP49008.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIJINE=22426070; PubMed=12537573; MEDIJINE=22426070; PubMed=12537573; Kaminker J.S., Bergman C.M., Kronmiller Patel S. Frise B., Wheeler D.A., Lewis Ashburner M., Celniker S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22426065; PubMed=12537568; Celniker S.E., Wheeler D.A., Kronm
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                                                                                                                                                                                                                                                                                                                                                                             Lewis S.B.;
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                                                                                                                                                                                     EQUENCE
               GO:0008450; F:O-sialoglycoprotein endopeptidase activity; GO:0008270; F:zinc ion binding; IEA.
GO:0006508; P:proteolysis and peptidolysis; IEA.
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E., Rubin
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Best Local S
Matches 83
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Pfam; PF00814; Peptidase M22; 1.
PIRSF; PIRSF004537; Osialg1c pptds; 1.
PRINTS; PR00789; OSIALOPTASE.
ProDom; PD002367; Peptidase M22; 1.
TIGRPAMS; TIGR00329; gcp; 1.
SEQUENCE 409 AA; 45328 MW; 9797F661
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O22145; Q8VWL2;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation updat
Yamada K., Banh J., C
Deng J.M., Goldsmith
Tang C., Toriumi M.,
                                                                                              Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jone Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Sato Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecke
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Sykes S.M., Mason
Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotytedons; core eudicots; rosids;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                      Submitted (MAR-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                             Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=At2g45270; Synonyms=GCP1;
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                                                                                                                                                                                                           K., Adamska I.;
(JAN-2001) to the
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son T.M., Kerlavage A.
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45328 MW; 9797F66B7D155538 CRC64;
                 Chan M.M.,
h A.D., Lee
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               Lee
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Pred. No. 6.9e-21;
 Chang C.
e J.M., On
Yamamura
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           C.H., Chang E
Onodera C.S.,
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TISSUB-Ploral meristem 5-10 days when regenerated in vitr Pan J.H., Ma Y., Zhang X.S.;
"Hyacinthus orientalis O-sialoglycoprotein endopeptidase mRNA, expressed during regeneration of floral bud.";
submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY389554; AAT08652.1; -.
InterPro; IPR000905; Peptidase M22.
PRINTS; PR00789; OSIALOPTASE.
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GO; GO:0008459; F:O-sialoglycoprotein endopeptidase GO; GO:0008273; F:peptidase activity; IEA.

GO; GO:0008270; F:zinc ion binding; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

InterPro; IPR001905; Peptidase M2.2

InterPro; IPR001905; Peptidase M2.2

PIRSF; PIRSF004537; Osialgl.

PIRSF; PIRSF004537; Osialgl. pptds; 1.
                                                                                                                                                                                                  Hyacinthus orientalis.
Eukaryota; Viridiplantae; Str.
Spermatophyta; Magnoliophyta;
                                                                                                                                                                                                                                                    25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
0-sialoglycoprotein endopeptidase (Fragment).
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Submitted (JUN-2002) to the
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Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lir
Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T.,
Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W.,
                                                                                                                                                                                   Hyacinthus
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ProDom; PD002367; Peptidase_N
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yta; Liliopsida; Asparagales; Hyacinthaceae;
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X Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
A Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
A Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
A Pohl T., Fortetelle D., Vandenbol M., Weidner S., Galibert F.;
T "Analysis of the chromosome sequence of the legume symbiont
Sinorhizobium meliloti strain 1021.";
T sinorhizobium meliloti strain 1021.";
EMBL; AL591792; CAC47657.1; -.
IR EMBL; AL591792; CAC47657.1; -.
IR GO; GO:0008450; F:O-sialoglycoprotein endopeptidase activity; IEA.
GO; GO:0008270; F:zinc ion binding; IEA.
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                                                                                                                                                                                                                                                         TIGRFAMS; TIGR00329; gcp; 1.
Complete proteome; Hydrolase.
SEQUENCE 360 AA; 37906 MW; A07F946AB562EA86 CRC64;
                                                                                                                                                                                                                                                                                                                                            Pfam; PF00014; Peptidase M22; 1.
PIRSF; PIRSF004537; OsialTglc pptds; 1.
PRINTS; PR00789; OSIALOPTASE.
ProDom; PD002367; Peptidase M22; 1.
TIGRFAMs; TIGR00329; gcp; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0006508; P:proteolysis and peptidolysis; IRA. InterPro; IPR000905; Peptidase M22. InterPro; IPR009180; Pept M22 Osialgl. Pfam; PF00814; Peptidase M22; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 ARAIEWALEIEPTVQ----CLVVSGGVASNKYVRSRLNHLVVKTGLRLVCPPPSLCTDNGV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127 HRAILFCKQRDLLPQNNAVLVASGGVASNFYIRRALBILTNATQCTLLCPPPRLCTDNGI 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               187 MIAWNGIERLRAGLGILHDIEGIRYEPKCPL 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 LGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFHFDIKPPLHHAKN
        N
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                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNFSYAGLK--TOVRLAIESRNICIDKSPISLATCHDRRMRADIAASFQQVAVLHLEDRC 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDFSFTGLQHVTDKIIMKKEKEEGIEKGQILSSA-----ADIAATVQHTMACHLVKRT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IGTTIDDAIGEAYDKTARWIGL-----DWGKGGGPALEELALEGDANSVKFKIPWRQHKD
    LALVQGVSDFLLLGKSLDIAPGDMLDKVARRLSLIKHPECSTMSGGKAIEHLAKQGNRFH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       255
255 AA;
                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               255
28516 MW; 529D22666C284106 CRC64;
                                                                                                                              21.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.2%; Score 299.5; DB 2; 37.4%; Pred. No. 3.3e-18;
                                                                                                32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26;
                                                                                       Score 262.5; DB Pred. No. 9e-15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                          DB 2;
                                                                                           85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79;
                                                                                       Indels 43;
                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                               CTLLCPPPRLCTDNGIMIAWNGIERLRAGLGILHDIEGIRYEPKC--PLGVDISKEVG 226
                                                                                                AATVOHTMACHLVKRTHRAILFCKORDLLPQNNAVLVASGGVASNFYIRRALEILTNATO 170
                                                                                                                                   FDFPRPLVGDARLDFSFSGLKTAVRQAAQSLGPVTDQDI------
FRFIAPPLQLCTDNAAMIAWAGAERLAAGL----PADGLDAAPRSRWPLDSEAKALIG 352
                                                                  CASFORAISRTLRDRVGRGLKRFR-ADFASVDQPALVVAGGVAANQTLRRTLQSLCDEHG
                                                                                                                                                                  PDIKPPLHHAKNCDFSFTGLQ------HVTDKIIMKKEKEEGIEKGQILSSAADI 110
                                                                  298
                                                                                                                                     239
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